GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 17:11:45 ; Search time 147.679 Seconds
(without alignments)
3569.936 Million cell updates/sec

Title: US-09-373-658C-2
Perfect score: 5189
Sequence: 1 MGNAERAPGSRSFGPVPTLL.....CDPLKKPKHFIDFCTMAECS 950

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09373658/runat_18062004_135343_10318/app_query.fasta_1.2254
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09373658_@CGN_1_1_156_@runat_18062004_135343_10318 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5189	100.0	4676	4	US-09-130-491-1	Sequence 1, Appli
	2	5176	99.7	4858	4	US-09-392-184-1	Sequence 1, Appli
	3	5174	99.7	3889	4	US-09-568-559-1	Sequence 1, Appli
	4	4287	82.6	3706	4	US-09-484-970B-58	Sequence 58, Appl
	5	3947	76.1	2184	4	US-09-445-023A-2	Sequence 2, Appli
	6	3677	70.9	2184	4	US-09-445-023A-13	Sequence 13, Appl
	7	2284.5	44.0	3638	4	US-09-369-364A-8	Sequence 8, Appli
c	8	2176.5	41.9	3126	4	US-09-392-184-7	Sequence 7, Appli
	9	2168	41.8	4192	4	US-09-122-126B-1	Sequence 1, Appli
	10	2168	41.8	4192	4	US-09-634-286A-1	Sequence 1, Appli
	11	1931	37.2	3250	4	US-09-122-126B-14	Sequence 14, Appl
	12	1931	37.2	3250	4	US-09-634-286A-14	Sequence 14, Appl
	13	1918	37.0	3002	4	US-09-369-364A-1	Sequence 1, Appli
	14	1756.5	33.9	5804	4	US-09-369-364A-12	Sequence 12, Appl
	15	1611	31.0	2625	4	US-09-369-364A-14	Sequence 14, Appl
	16	1405.5	27.1	2114	4	US-09-130-491-7	Sequence 7, Appli
c	17	1320.5	25.4	5357	4	US-09-392-184-5	Sequence 5, Appli
	18	1296.5	25.0	3675	4	US-09-930-872-3	Sequence 3, Appli
	19	1296.5	25.0	4042	4	US-09-930-872-5	Sequence 5, Appli
	20	1213.5	23.4	2727	4	US-09-963-791-1	Sequence 1, Appli
	21	1210.5	23.3	3218	4	US-09-369-364A-6	Sequence 6, Appli
	22	1198	23.1	3885	4	US-09-369-364A-16	Sequence 16, Appl
	23	1152.5	22.2	2274	4	US-09-963-791-23	Sequence 23, Appl
	24	1134	21.9	6692	4	US-09-491-522-1	Sequence 1, Appli
	25	1118	21.5	4580	4	US-09-491-522-8	Sequence 8, Appli
	26	1065.5	20.5	3160	4	US-09-963-791-25	Sequence 25, Appl
	27	1041.5	20.1	1520	4	US-09-369-364A-3	Sequence 3, Appli
	28	1037.5	20.0	2848	4	US-09-369-364A-4	Sequence 4, Appli
	29	966.5	18.6	2450	4	US-09-491-522-2	Sequence 2, Appli
	30	965.5	18.6	2450	4	US-09-491-522-9	Sequence 9, Appli
	31	780	15.0	1770	4	US-09-963-791-11	Sequence 11, Appl
	32	719	13.9	1317	4	US-09-963-791-21	Sequence 21, Appl
	33	716.5	13.8	739	4	US-09-369-364A-10	Sequence 10, Appl
c	34	641	12.4	1810	4	US-09-833-381-1056	Sequence 1056, Ap
	35	612.5	11.8	703	4	US-09-392-184-6	Sequence 6, Appli
	36	601	11.6	5720	4	US-09-800-729-18	Sequence 18, Appl
	37	592.5	11.4	1524	4	US-09-963-791-9	Sequence 9, Appli
	38	574.5	11.1	1803	4	US-09-369-364A-20	Sequence 20, Appl
	39	531.5	10.2	1071	4	US-09-963-791-19	Sequence 19, Appl
	40	508	9.8	2023	4	US-09-491-522-6	Sequence 6, Appli
	41	498	9.6	1407	4	US-09-963-791-5	Sequence 5, Appli
	42	486	9.4	1476	4	US-09-930-872-1	Sequence 1, Appli
	43	440	8.5	852	4	US-09-800-729-54	Sequence 54, Appl
	44	438	8.4	3559	4	US-09-800-729-53	Sequence 53, Appl
	45	437	8.4	954	4	US-09-963-791-15	Sequence 15, Appl

ALIGNMENTS

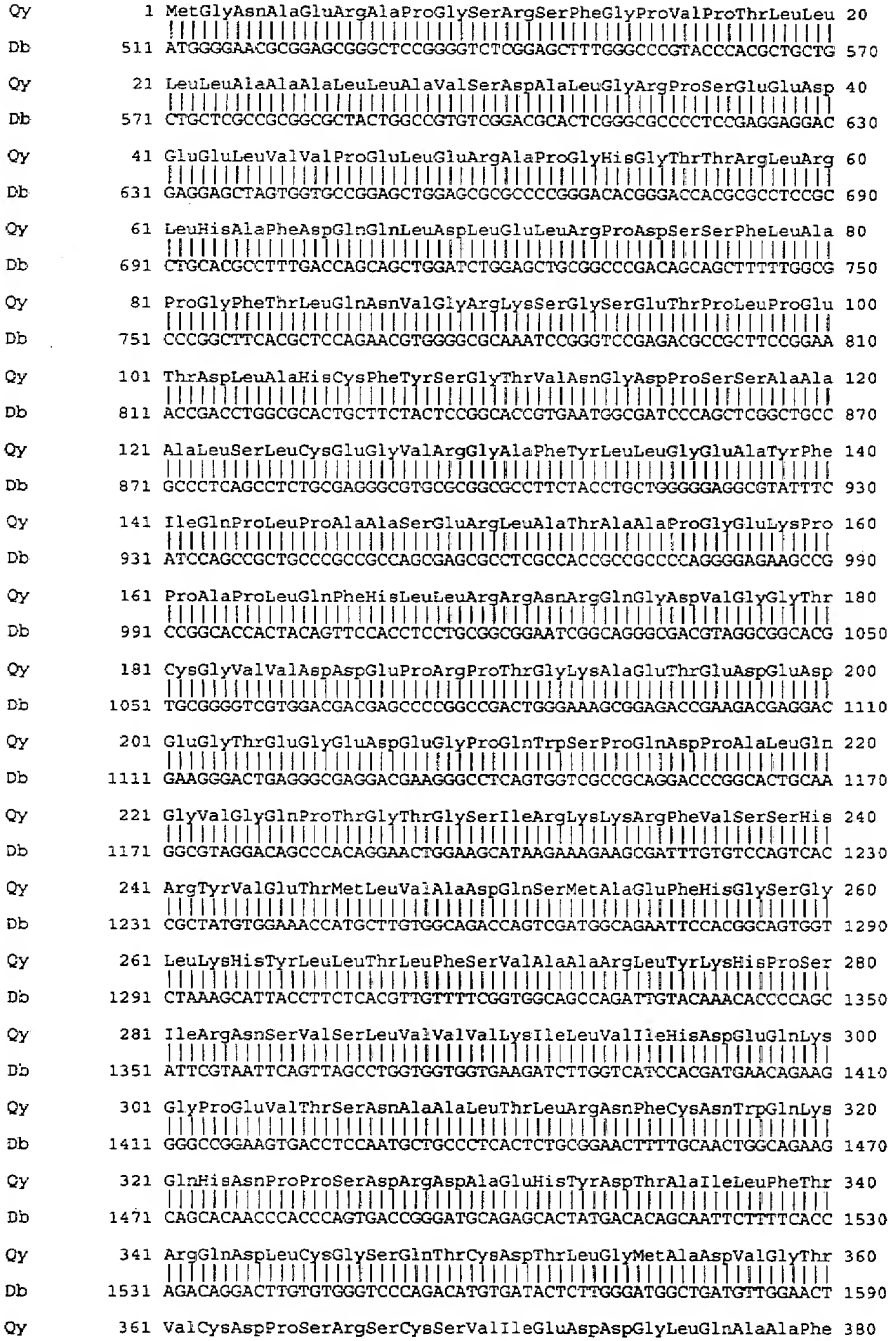
RESULT 1
US-09-130-491-1
; Sequence 1, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-~~07~~ 06
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-09-130-491-1

no biotech data on for TANGO-1
no bio tech data on for TANGO 1
not correct invention
60/054, 966

Alignment Scores:

Pred. No.:	0	Length:	4676
Score:	5189.00	Matches:	950
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-373-658C-2 (1-950) x US-09-130-491-1 (1-4676)


Qy 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db 511 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 570
Qy 21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
Db 571 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 630
Qy 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
Db 631 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 690
Qy 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
Db 691 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 750
Qy 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db 751 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 810
Qy 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db 811 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 870
Qy 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
Db 871 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 930
Qy 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
Db 931 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 990
Qy 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
Db 991 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 1050
Qy 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db 1051 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 1110
Qy 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db 1111 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 1170
Qy 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
Db 1171 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1230
Qy 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db 1231 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1290
Qy 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
Db 1291 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1350
Qy 281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
Db 1351 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1410
Qy 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db 1411 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTGCAACTGGCAGAAG 1470
Qy 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
Db 1471 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1530
Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db 1531 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1590
Qy 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
Db 1591 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1650
Qy 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
Db 1651 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1710
Qy 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db 1711 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1770
Qy 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
Db 1771 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1830
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db 1831 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1890
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db 1891 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1950
Qy 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
Db 1951 CACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 2010
Qy 501 ValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db 2011 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 2070
Qy 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
Db 2071 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 2130
Qy 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
Db 2131 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 2190
Qy 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
Db 2191 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 2250
Qy 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
Db 2251 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 2310
Qy 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
Db 2311 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2370
Qy 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
Db 2371 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2430
Qy 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db 2431 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2490
Qy 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
Db 2491 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2550
Qy 681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700
Db 2551 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2610
Qy 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db 2611 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2670
Qy 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740

```
Db       2671 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2730

Qy        741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760

Db       2731 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2790

Qy        761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780

Db       2791 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2850

Qy        781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800

Db       2851 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2910

Qy        801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820

Db       2911 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2970

Qy        821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840

Db       2971 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 3030

Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860

Db       3031 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 3090

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880

Db       3091 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 3150

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900

Db       3151 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 3210

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920

Db       3211 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 3270

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940

Db       3271 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 3330

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950

Db       3331 ATAGACTTTTGCACAATGGCAGAATGCAGT 3360

RESULT 2
US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN
;  TITLE OF INVENTION:  PROTEASE HOMOLOGS
;  FILE REFERENCE:  5800-55
;  CURRENT APPLICATION NUMBER: US/09/392,184
;  CURRENT FILING DATE:  1999-09-09
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 4858
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(4858)
;   OTHER INFORMATION: reprolysin (ADAM family of metalloprotease)
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(4858)
;   OTHER INFORMATION: n = A,T,C or G
US-09-392-184-1

Alignment Scores:

Pred. No.:                0                Length:          4858
Score:                    5176.00          Matches:         950
Percent Similarity:       99.89%           Conservative:    0
Best Local Similarity:    99.89%           Mismatches:      0
Query Match:              99.75%           Indels:          1
DB:                       4                Gaps:            0

US-09-373-658C-2 (1-950) x US-09-392-184-1 (1-4858)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20

Db        505 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 564

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40

Db        565 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 624

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60

Db        625 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 684

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80

Db        685 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 744

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100

Db        745 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 804

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120

Db        805 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 864

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140

Db        865 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 924

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160

Db        925 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 984

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180

Db        985 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 1044

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200

Db       1045 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 1104

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220

Db       1105 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 1164

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240

Db       1165 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1224

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260

Db       1225 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1284

Qy        261 LeuLysHisTyrLeuLeu-ThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSe 280

Db       1285 CTAAAGCATTACCTTCTCAACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAG 1344

Qy        280 rIleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLy 300

Db       1345 CATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAA 1404

Qy        300 sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLy 320

Db       1405 GGGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAA 1464
```

```
Qy       320 sGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheTh 340
Db      1465 GCAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCAC 1524

Qy       340 rArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyTh 360
Db      1525 CAGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAAC 1584

Qy       360 rValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPh 380
Db      1585 TGTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTT 1644

Qy       380 eThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCy 400
Db      1645 CACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTG 1704

Qy       400 sAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLe 420
Db      1705 TGCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCT 1764

Qy       420 uAspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAs 440
Db      1765 GGACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAA 1824

Qy       440 nGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLe 460
Db      1825 TGGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCT 1884

Qy       460 uProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLy 480
Db      1885 CCCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAA 1944

Qy       480 sHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGl 500
Db      1945 ACACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGG 2004

Qy       500 yValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGl 520
Db      2005 GGTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGG 2064

Qy       520 yLysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPr 540
Db      2065 GAAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCC 2124

Qy       540 oPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGl 560
Db      2125 TTTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGG 2184

Qy       560 yGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTy 580
Db      2185 AGGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTA 2244

Qy       580 rCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAs 600
Db      2245 CTGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAA 2304

Qy       600 nGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPh 620
Db      2305 TGGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTT 2364

Qy       620 eGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspAr 640
Db      2365 TGGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAG 2424

Qy       640 gCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVa 660
Db      2425 GTGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGT 2484

Qy       660 lValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVa 680
Db      2485 TGTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGT 2544

Qy       680 lLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCy 700
Db      2545 AAAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTG 2604

Qy       700 sGlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGl 720
Db      2605 CGGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGG 2664

Qy       720 yTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAs 740
Db      2665 ATATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAA 2724

Qy       740 nGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTy 760
Db      2725 CCAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATA 2784

Qy       760 rIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVa 780
Db      2785 TATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGT 2844

Qy       780 lValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLe 800
Db      2845 TGTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCT 2904

Qy       800 uLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLy 820
Db      2905 CAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAA 2964

Qy       820 sTyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAl 840
Db      2965 ATACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGC 3024

Qy       840 aTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgAr 860
Db      3025 ATGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAG 3084

Qy       860 gLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLy 880
Db      3085 ACTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAA 3144

Qy       880 sProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTr 900
Db      3145 GCCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTG 3204

Qy       900 pSerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSe 920
Db      3205 GTCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTC 3264

Qy       920 rHisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPh 940
Db      3265 CCATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTT 3324

Qy       940 eIleAspPheCysThrMetAlaGluCysSer 950
Db      3325 CATAGACTTTTGCACAATGGCAGAATGCAGT 3355
```

RESULT 3
US-09-568-559-1
; Sequence 1, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PastSEQ for Windows Version 4.0

; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-09-568-559-1

Alignment Scores:

Pred. No.:	0	Length:	3889
Score:	5174.00	Matches:	948
Percent Similarity:	99.79%	Conservative:	0
Best Local Similarity:	99.79%	Mismatches:	2
Query Match:	99.71%	Indels:	0
DB:	4	Gaps:	0

US-09-373-658C-2 (1-950) x US-09-568-559-1 (1-3889)

```
Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         59 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 118

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CTGCTCGCGGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 178

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 238

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 298

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 358

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 418

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 478

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 538

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACG 598

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 658

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
              |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        659 GAAGGGACTGAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 718

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 778

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 838

Qy        261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 898

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 958

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1018

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1078

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1138

Qy        361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1198

Qy        381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1258

Qy        401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1318

Qy        421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1378

Qy        441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1438

Qy        461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1498

Qy        481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1558

Qy        501 ValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGly 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1618

Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCCACAGAAAGCATTTTGATACGCCT 1678

Qy        541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1738

Qy        561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 1798

Qy        581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1799 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 1858

Qy        601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1859 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 1918

Qy        621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1919 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 1978

Qy        641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1979 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2038

Qy        661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680

Db       2039 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2098

Qy        681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700

Db       2099 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2158

Qy        701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720

Db       2159 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2218

Qy        721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740

Db       2219 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2278

Qy        741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760

Db       2279 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2338

Qy        761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780

Db       2339 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2398

Qy        781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800

Db       2399 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2458

Qy        801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820

Db       2459 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2518

Qy        821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840

Db       2519 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2578

Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860

Db       2579 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2638

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880

Db       2639 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2698

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900

Db       2699 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2758

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920

Db       2759 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 2818

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940

Db       2819 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 2878

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950

Db       2879 ATAGACTTTTGCACAATGGCAGAATGCAGT 2908

RESULT 4
US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;  APPLICANT:  Jones, Karen A.
;  APPLICANT:  Volkmuth, Wayne
;  APPLICANT:  Walker, Michael G.
;  TITLE OF INVENTION:  BONE REMODELING GENES
;  FILE REFERENCE:  PB-0014 US
;  CURRENT APPLICATION NUMBER: US/09/484,970B
;  CURRENT FILING DATE:  2000-01-18
;  NUMBER OF SEQ ID NOS:  172
;  SOFTWARE:  PERL Program
; SEQ ID NO 58
;   LENGTH: 3706
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6426186 007074.1
;   NAME/KEY: unsure
;   LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
;   OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Alignment Scores:
Pred. No.:                0                Length:          3706
Score:                    4287.00          Matches:         777
Percent Similarity:       99.87%           Conservative:    0
Best Local Similarity:    99.87%           Mismatches:      0
Query Match:              82.62%           Indels:          1
DB:                       4                Gaps:            0

US-09-373-658C-2 (1-950) x US-09-484-970B-58 (1-3706)

Qy        174 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 193

Db          3 CAGGGCGACGTAGGCGGCACGTGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAA 62

Qy        194 AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer 213

Db         63 GCGGAGACCGAAGACGAGGACGAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCG 122

Qy        214 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 233

Db        123 CCGCAGGACCCGGCACTGCAAGGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAG 182

Qy        234 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 253

Db        183 AAGCGATTTGTGTCCAGTCACCGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATG 242

Qy        254 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 273

Db        243 GCAGAATTCCACGGCAGTGGTCTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCC 302

Qy        274 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeu 293

Db        303 AGATTGTACAAACACCCCAGCATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTG 362

Qy        294 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 313

Db        363 GTCATCCACGATGAACAGAAGGGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGG 422

Qy        314 AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 333

Db        423 AACTTTTGCAACTGGCAGAAGCAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTAT 482

Qy        334 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 353

Db        483 GACACAGCAATTCTTTTCACCAGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTT 542

Qy        354 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 373

Db        543 GGGATGGCTGATGTTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGAT 602

Qy        374 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 393

Db        603 GATGGTTTACAAGCTGCCTTCACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCA 662

Qy        394 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 413

Db        663 CATGATGATGCAAAGCAGTGTGCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATG 722
```

```
Qy       414 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMet 433
Db       723 GCGTCAATGCTTTCCAACCTGGACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATG 782

Qy       434 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 453
Db       783 ATTACATCATTTCTGGATAATGGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCC 842

Qy       454 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 473
Db       843 ATACAGCTCCCAGGCGATCTCCCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTT 902

Qy       474 ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp 493
Db       903 ACATTTGGGGAGGACTCCAAACACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGG 962

Qy       494 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProProTrpAlaAsp 513
Db       963 TGTACCGGCACCTCTGGTGGGGTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGAT 1022

Qy       514 GlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThrAsp 533
Db      1023 GGCACCAGCTGTGGAGAAGGGAAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGAC 1082

Qy       534 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 553
Db      1083 AGAAAGCATTTTGATACGCCTTTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGAC 1142

Qy       554 CysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 573
Db      1143 TGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTC 1202

Qy       574 ProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 593
Db      1203 CCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTT 1262

Qy       594 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsn 613
Db      1263 GAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAAC 1322

Qy       614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAla 633
Db      1323 GAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCT 1382

Qy       634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 653
Db      1383 GGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTC 1442

Qy       654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673
Db      1443 TTCGTTTTGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTC 1502

Qy       674 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 693
Db      1503 TGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAG 1562

Qy       694 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySer 713
Db      1563 TTTGATAAATGTGGTGTTTGCGGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCA 1622

Qy       714 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 733
Db      1623 GTTACTAGTGCAAAACCTGGATATCATGATATCATCACAATTCCAACTGGAGCCACCAAC 1682

Qy       734 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIl 753
Db      1683 ATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGGCAGCTTTCTTGCCAT 1742

Qy       753 eLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGl 773
Db      1743 CAAAGCTGCTGATGGCACATATATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCA 1802

Qy       773 nAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluAr 793
```

```
Db      1803 AGACATTATGTACAAAGGTGTTGTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAG 1862

Qy       793 gIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 813
Db      1863 AATTCGCAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAA 1922

Qy       813 nAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPheAs 833
Db      1923 TGCCCTTCGACCTAAAATTAAATACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAA 1982

Qy       833 nAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCy 853
Db      1983 TGCTATCCCCACTTTTTCAGCATGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATG 2042

Qy       853 sGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSe 873
Db      2043 TGAATTGGGTTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTC 2102

Qy       873 rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 893
Db      2103 CGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCC 2162

Qy       893 oGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLy 913
Db      2163 CCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAA 2222

Qy       913 sArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAspPr 933
Db      2223 AAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCC 2282

Qy       933 oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950
Db      2283 TTTAAAGAAACCTAAACATTTCATAGACTTTTGCACAATGGCAGAATGCAGT 2334
```

RESULT 5
US-09-445-023A-2
; Sequence 2, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS-
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-2

Alignment Scores:

Pred. No.:	0	Length:	2184
Score:	3947.00	Matches:	712
Percent Similarity:	99.44%	Conservative:	4
Best Local Similarity:	98.89%	Mismatches:	4
Query Match:	76.06%	Indels:	0
DB:	4	Gaps:	0

US-09-373-658C-2 (1-950) x US-09-445-023A-2 (1-2184)

```
Qy        231 IleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAsp 250
              :::|||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db         22 CTTAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTTGTGGCAGAC 81

Qy        251 GlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSer 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCATTACCTTCTCACGTTGTTTTCG 141

Qy        271 ValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 GTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAATTCAGTTAGCCTGGTGGTGGTG 201

Qy        291 LysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeu 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAAGTGACCTCCAATGCTGCCCTC 261

Qy        311 ThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAla 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 ACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAACCCACCCAGTGACCGGGATGCA 321

Qy        331 GluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCys 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 GAGCACTATGACACAGCAATTCTTTTCACCAGACAGGACTTGTGTGGGTCCCAGACATGT 381

Qy        351 AspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerVal 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTC 441

Qy        371 IleGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPhe 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCCCATGAATTAGGCCACGTGTTT 501

Qy        391 AsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSer 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 AACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTTAATGGTGTGAACCAGGATTCC 561

Qy        411 HisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSer 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGCCAGCCTTGGTCTCCTTGCAGT 621

Qy        431 AlaTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysPro 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 GCCTACATGATTACATCATTTCTGGATAATGGTCATGGGGAATGTTTGATGGACAAGCCT 681

Qy        451 GlnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGln 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACCTTGTACGATGCCAACCGGCAG 741

Qy        471 CysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSer 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCCGATGCAGCCAGCACATGTAGC 801

Qy        491 ThrLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProPro 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 ACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTGTGTCAAACCAAACACTTCCCG 861

Qy        511 TrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsn 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGTATCAACGGCAAGTGTGTGAAC 921

Qy        531 LysThrAspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 AAAACCGACAGGAAGCATTTTGATACGCCTTTTCATGGAAGCTGGGGACCATGGGGACCG 981

Qy        551 TrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAsp 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGAC 1041

Qy        571 AsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSer 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 AACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAGATCC 1101

Qy        591 CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGlu 610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 TGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATGTGAA 1161

Qy        611 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIlePro 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 GCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGATTCCC 1221

Qy        631 LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 AAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATT 1281

Qy        651 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 GGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTTGATGGTACTCCATGTAGCCCAGATTCC 1341

Qy        671 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSer 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 ACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGACTCC 1401

Qy        691 LysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIle 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 AAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAATGGATCTACTTGTAAAAAAATA 1461

Qy        711 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 730
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1462 TCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGATATCGTCACAATTCCAACTGGA 1521

Qy        731 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 GCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGCAGCTTT 1581

Qy        751 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1582 CTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAATGGTGACTACACTTTGTCCACC 1641

Qy        771 LeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1642 TTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGGTACAGCGGCTCCTCTGCGGCA 1701

Qy        791 LeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThr 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1702 TTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACT 1761

Qy        811 ValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGlu 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1762 GTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTACTTCGTAAAGAAGAAGAAGGAA 1821

Qy        831 SerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSer 850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1822 TCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATTGAAGAGTGGGGCGAATGTTCT 1881

Qy        851 LysSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGln 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1882 AAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAG 1941

Qy        871 ProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHis 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1942 CCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGACCAT 2001

Qy        891 ProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGly 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2002 CCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAAGGGT 2061

Qy        911 TyrLysLysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSer 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2062 TACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGC 2121

Qy        931 CysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950
              ||||||||||||||||||||||||||||||||||||||||||||||||:::  :::||||||
Db       2122 TGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTTTGCACACTGACACAGTGCAGT 2181
```

```
RESULT 6
US-09-445-023A-13
; Sequence 13, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
;  APPLICANT: Hirose, Kunitaka
;  APPLICANT:  Inoguchi, Eiji
;  APPLICANT:  Hakozaki, Michinori
;  APPLICANT:  Ishioka, Keiko
;  APPLICANT:  Ishida, Yukako
;  APPLICANT:  Matsushima, Kouji
;  APPLICANT:  Kuno, Kouji
;  TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
;  TITLE OF INVENTION:  composition and method of immunologically analyzing human ADAMTS
;  FILE REFERENCE: Q57092
;  CURRENT APPLICATION NUMBER: US/09/445,023A
;  CURRENT FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER: JP 9-160422
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 2184
;   TYPE: DNA
;   ORGANISM: Mus sp.
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(2184)
US-09-445-023A-13

Alignment Scores:
Pred. No.:                0          Length:          2184
Score:                    3677.00    Matches:         651
Percent Similarity:       95.32%     Conservative:    42
Best Local Similarity:    89.55%     Mismatches:      34
Query Match:              70.86%     Indels:          0
DB:                       4          Gaps:            0

US-09-373-658C-2 (1-950) x US-09-445-023A-13 (1-2184)

Qy        224 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 243
              :::|||:::|||  |||||||||||||||||||||||||||||||||||  ||||||||||
Db          1 AAGCCATCAGGACCAGGAAGCATAAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTG 60

Qy        244 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 263
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db         61 GAAACCATGCTCGTAGCTGACCAGTCCATGGCCGACTTCCACGGCAGCGGTCTAAAGCAT 120

Qy        264 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 283
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        121 TACCTTCTAACCCTGTTCTCGGTGGCAGCCAGGTTTTACAAGCATCCCAGCATTAGGAAT 180

Qy        284 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 303
              |||:::|||||||||||||||||||||||||||||:::::|||||||||||||||||||
Db        181 TCAATTAGCCTGGTGGTGGTGAAGATCTTGGTCATATACGAGGAGCAGAAGGGACCAGAA 240

Qy        304 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 323
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        241 GTTACCTCCAATGCAGCTCTCACCCTTCGGAATTTCTGCAGCTGGCAGAAACAACACAAC 300

Qy        324 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 343
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCCCCAGTGACCGGGATCCAGAGCACTATGACACTGCAATTCTGTTCACCAGACAGGAT 360

Qy        344 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 363
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTATGTGGCTCCCACACGTGTGACACTCTCGGAATGGCAGATGTTGGAACCGTATGTGAC 420

Qy        364 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCAGCAGGAGCTGCTCAGTCATAGAAGATGATGGTTTGCAAGCTGCCTTCACCACAGCC 480

Qy        384 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CATGAATTGGGCCATGTGTTTAACATGCCGCACGATGATGCTAAGCACTGTGCCAGCTTG 540

Qy        404 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 423
              |||||||||:::  |||||||||:::|||||||||||||||||||:::|||||||||||
Db        541 AATGGTGTGAGTGGCGATTCTCATCTGATGGCCTCGATGCTCTCCAGCTTAGACCATAGC 600

Qy        424 GlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsnGlyHisGly 443
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        601 CAGCCCTGGTCACCTTGCAGTGCCTACATGGTCACGTCCTTCCTAGATAATGGACACGGG 660

Qy        444 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 463
              ||||||||||||||||||||||||||||||||||:::|||||  |||||||||||||||
Db        661 GAATGTTTGATGGACAAGCCCCAGAATCCAATCAAGCTCCCTTCTGATCTTCCCGGTACC 720

Qy        464 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 483
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db        721 TTGTACGATGCCAACCGCCAGTGTCAGTTTACATTCGGAGAGGAATCCAAGCACTGCCCT 780

Qy        484 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 503
              ||||||||||||||||||:::|||||||||||||||||||||||||||:::||||||||
Db        781 GATGCAGCCAGCACATGTACTACCCTGTGGTGCACTGGCACCTCCGGTGGCTTACTGGTG 840

Qy        504 CysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGCCAAACAAAACACTTCCCTTGGGCAGATGGCACCAGCTGTGGAGAAGGGAAGTGGTGT 900

Qy        524 IleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrProPheHisGly 543
              ::::::|||||||||||||||||||||||  ||||||||  ||||||  ||||||||||
Db        901 GTCAGTGGCAAGTGCGTGAACAAGACAGACATGAAGCATTTTGCTACTCCTGTTCATGGA 960

Qy        544 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 563
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGGGGACCATGGGGACCGTGGGGAGACTGCTCAAGAACCTGTGGTGGTGGAGTTCAA 1020

Qy        564 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACACAATGAGAGAATGTGACAACCCAGTCCCAAAGAACGGAGGGAAGTACTGTGAAGGC 1080

Qy        584 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 603
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db       1081 AAACGAGTCCGCTACAGGTCCTGTAACATCGAGGACTGTCCAGACAATAACGGAAAAACG 1140

Qy        604 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1141 TTCAGAGAGGAGCAGTGCGAGGCGCACAATGAGTTTTCCAAAGCTTCCTTTGGGAATGAG 1200

Qy        624 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 643
              |||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCACTGTAGAGTGGACACCCAAGTACGCCGGCGTCTCGCCAAAGGACAGGTGCAAGCTC 1260

Qy        644 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 663
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ACCTGTGAAGCCAAAGGCATTGGCTACTTTTTCGTCTTACAGCCCAAGGTTGTAGATGGC 1320

Qy        664 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACTCCCTGTAGTCCAGACTCTACCTCTGTCTGTGTGCAAGGGCAGTGTGTGAAAGCTGGC 1380

Qy        684 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAGTGTGGCGTTTGTGGAGGAAAC 1440

Qy        704 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 723
              |||||||||||||||||:::||||||  |||||||||  :::|||||||||||||||||
Db       1441 GGTTCCACATGCAAGAAGATGTCAGGAATAGTCACTAGTACAAGACCTGGGTATCATGAC 1500

Qy        724 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 743
              |||:::|||||||||  ||||||||||||||||||||||||  ||||||||||||||||
Db       1501 ATTGTCACAATTCCTGCTGGAGCCACCAACATTGAAGTGAAACATCGGAATCAAAGGGGG 1560

Qy        744 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 763
              ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
```

```
Db       1561 TCCAGAAACAATGGCAGCTTTCTGGCTATTAGAGCCGCTGATGGTACCTATATTCTGAAT 1620

Qy        764 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 783

Db       1621 GGAAACTTCACTCTGTCCACACTAGAGCAAGACCTCACCTACAAAGGTACTGTCTTAAGG 1680

Qy        784 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 803

Db       1681 TACAGTGGTTCCTCGGCTGCGCTGGAAAGAATCCGCAGCTTTAGTCCACTCAAAGAACCC 1740

Qy        804 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 823

Db       1741 TTAACCATCCAGGTTCTTATGGTAGGCCATGCTCTCCGACCCAAAATTAAATTCACCTAC 1800

Qy        824 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 843

Db       1801 TTTATGAAGAAGAAGACAGAGTCATTCAACGCCATTCCCACATTTTCTGAGTGGGTGATT 1860

Qy        844 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 863

Db       1861 GAAGAGTGGGGGGAGTGCTCCAAGACATGCGGCTCAGGTTGGCAGAGAAGAGTAGTGCAG 1920

Qy        864 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 883

Db       1921 TGCAGAGACATTAACGGACACCCTGCTTCCGAATGTGCAAAGGAAGTGAAGCCAGCCAGT 1980

Qy        884 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 903

Db       1981 ACCAGACCTTGTGCAGACCTTCCTTGCCCACACTGGCAGGTGGGGGATTGGTCACCATGT 2040

Qy        904 SerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSerHisAspGly 923

Db       2041 TCCAAAACTTGCGGGAAGGGTTACAAGAAGAGAACCTTGAAATGTGTGTCCCACGATGGG 2100

Qy        924 GlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPheIleAspPhe 943

Db       2101 GGCCTGTTATCAAATGAGAGCTGTGATCCTTTGAAGAAGCCAAAGCATTACATTGACTTT 2160

Qy        944 CysThrMetAlaGluCysSer 950

Db       2161 TGCACACTGACACAGTGCAGT 2181
```

RESULT 7
US-09-369-364A-8
; Sequence 8, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3638
; TYPE: DNA
; ORGANISM: Mus musculus ADAMTS-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (278)..(2992)
; NAME/KEY: misc_feature
; LOCATION: (3636)
; OTHER INFORMATION: n = T
US-09-369-364A-8

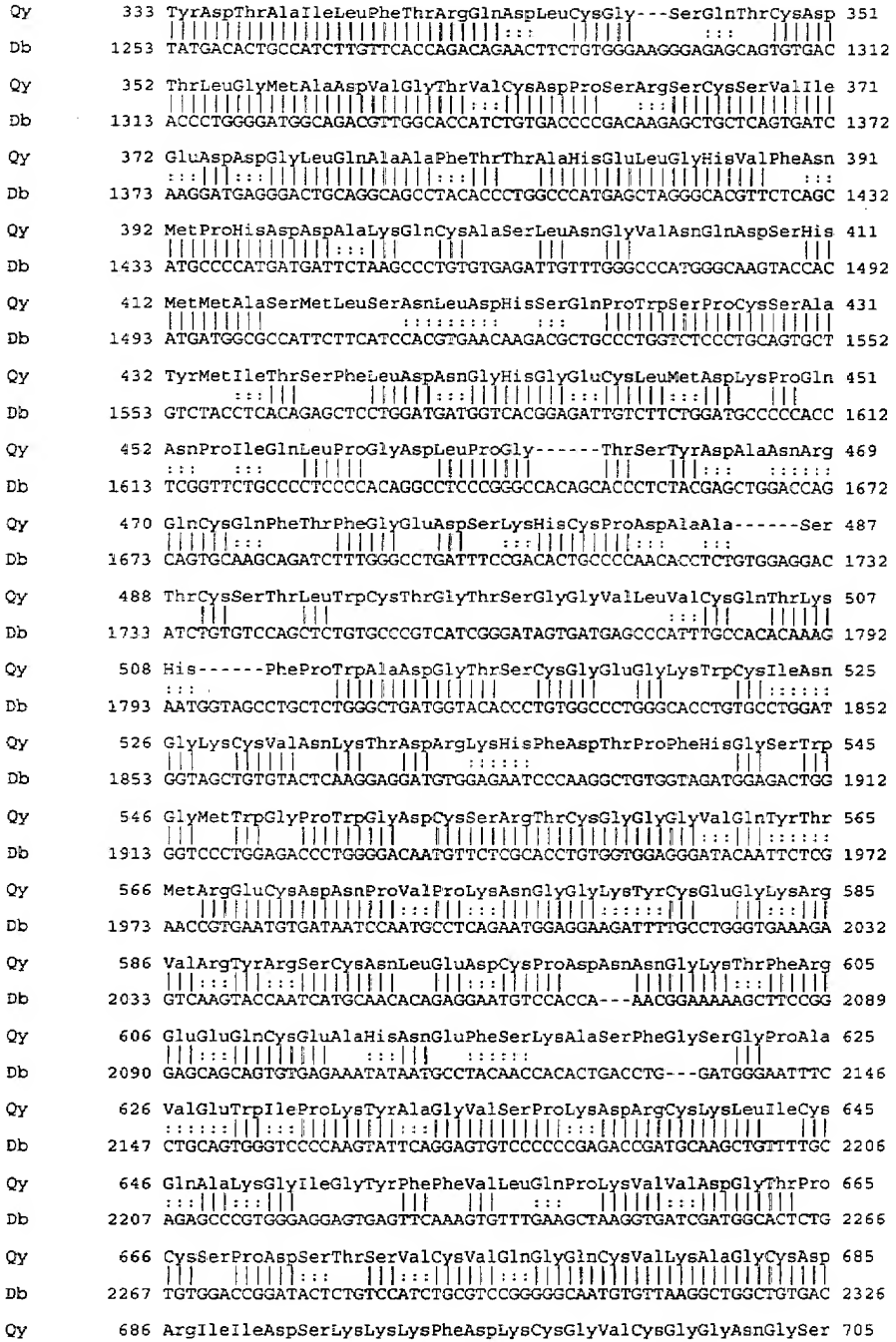
Alignment Scores:

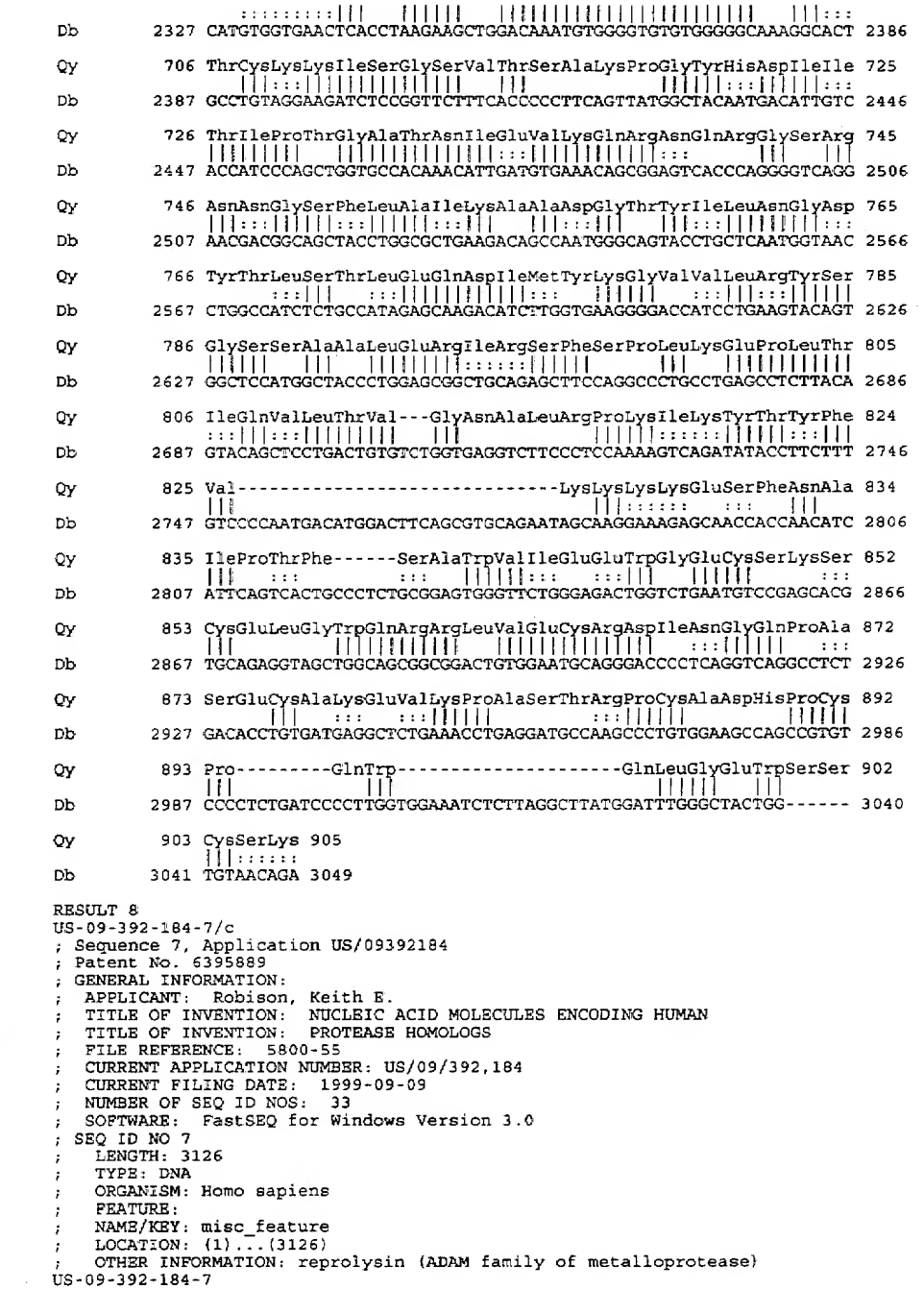
Pred. No.:	8.44e-201	Length:	3638
Score:	2284.50	Matches:	449
Percent Similarity:	63.10%	Conservative:	146
Best Local Similarity:	47.61%	Mismatches:	265

Query Match: 44.03% Indels: 83
DB: 4 Gaps: 21

US-09-373-658C-2 (1-950) x US-09-369-364A-8 (1-3638)

```
Qy         17 ProThrLeuLeuLeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgPro 36

Db        308 CCGCCCCTCCTGCTGCTGCTATTGCAGCTGCCGCCGCCGCCACTCGTCTGCGGAGCCCCG 367

Qy         37 Ser---------------GluGluAspGluGluLeuValValProGluLeuGluArgAla 51

Db        368 GCGGGGCCGGGAACCGGGGCGCAGGCCTCGGAGCTAGTGGTGCCC------ACGCGGTTG 421

Qy         52 ProGlyHisGlyThr---ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeu 70

Db        422 CCCGGCAGCGCGAGCGAGCTCGCCTTCCACCTGTCCGCCTTCGGCCAGGGCTTCGTGCTG 481

Qy         71 GluLeuArgProAspSerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArg 90

Db        482 CGCCTGGCGCCTGACGCCAGCTTCCTGGCGCCGGAATTCAAGATCGAGCGCCTCGGGGGC 541

Qy         91 LysSerGlySerGluThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGly 110

Db        542 TCGAGCGCGGCGGCCGGG------GGCGAGCCGGGACTGCGTGGCTGCTTCTTCTCTGGC 595

Qy        111 ThrValAsnGlyAspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGly 130

Db        596 ACAGTGAATGGAGAACGGGAGTCGCTGGCGGCGATGAGCTGTGTCGCGGGCTGGAGCGGC 655

Qy        131 AlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnProLeuProAlaAlaSer------ 148

Db        656 TCGTTCTTGCTGGCAGGCGAGGAGTTCACCATCCAGCCACAGGGCGCTGGGGACTCCCTG 715

Qy        149 ---------GluArgLeuAlaThrAlaAlaProGlyGluLysPro--------------- 160

Db        716 GACCAGCCTCATCGCCTGCAGCGCTGGGGGCCGGGACAGCGCCGCGAAGACCCCGGGCTC 775

Qy        161 ------------------------ProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172

Db        776 GCTGCCGCCGAAGTTTTCCCCCTCCCTCAAGGACTGGAGTGGGAGGTGGAGATGGGTAAT 835

Qy        173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192

Db        836 GGGCAGGGACAG---------------------------------------------- 847

Qy        193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212

Db        848 ------GAGAGAAGTGACAACGAAGAGGACAAGAAGCAGGACAAGGAGGGGTTGCTCAAA 901

Qy        213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232

Db        902 GAGACAGAAGACTCC------CGCAAAGTGCCACCACCCTTCGGATCC---AAAACTAGA 952

Qy        233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252

Db        953 AGCAAGAGGTTTGTGTCCGAGGCTCGCTTCGTGGAAACACTTCTGGTGGCTGATGCGTCC 1012

Qy        253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272

Db       1013 ATGGCTGCCTTCTATGGGACCGACCTGCAGAACCACATCCTCACGGTGATGTCAATGGCA 1072

Qy        273 AlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIle 292

Db       1073 GCCCGAATCTACAAGCACCCGAGCATCAGGAACTCCGTCAACCTTGTGGTGGTGAAAGTG 1132

Qy        293 LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeu 312

Db       1133 CTAATAGTGGAAAAAGAAAGATGGGGCCCGGAAGTGTCCGACAACGGGGGGCTCACACTG 1192

Qy        313 ArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis 332

Db       1193 CGCAACTTCTGCAGCTGGCAACGGCGTTTCAACAAGCCCAGTGACCGCCACCCGGAGCAC 1252
```



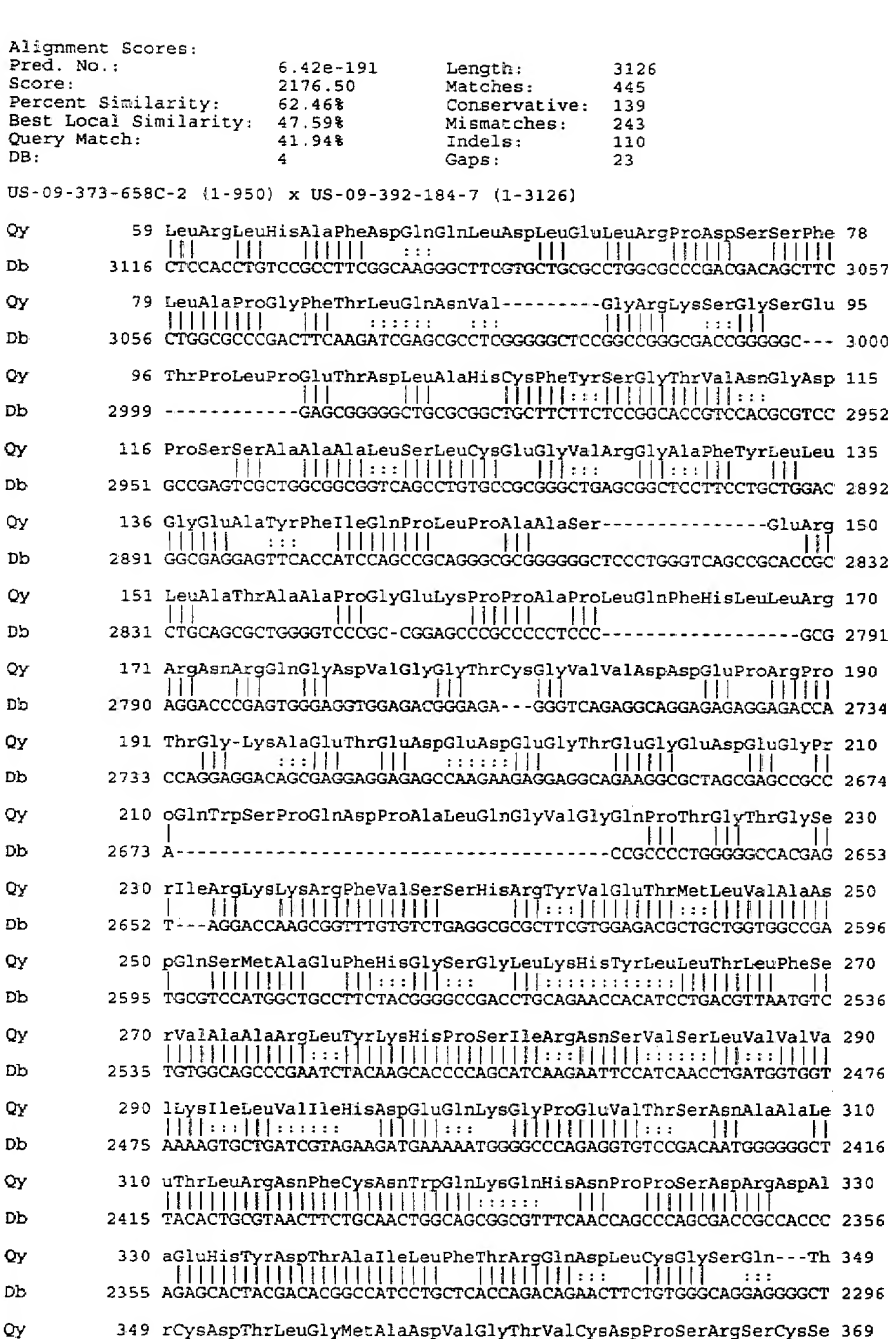


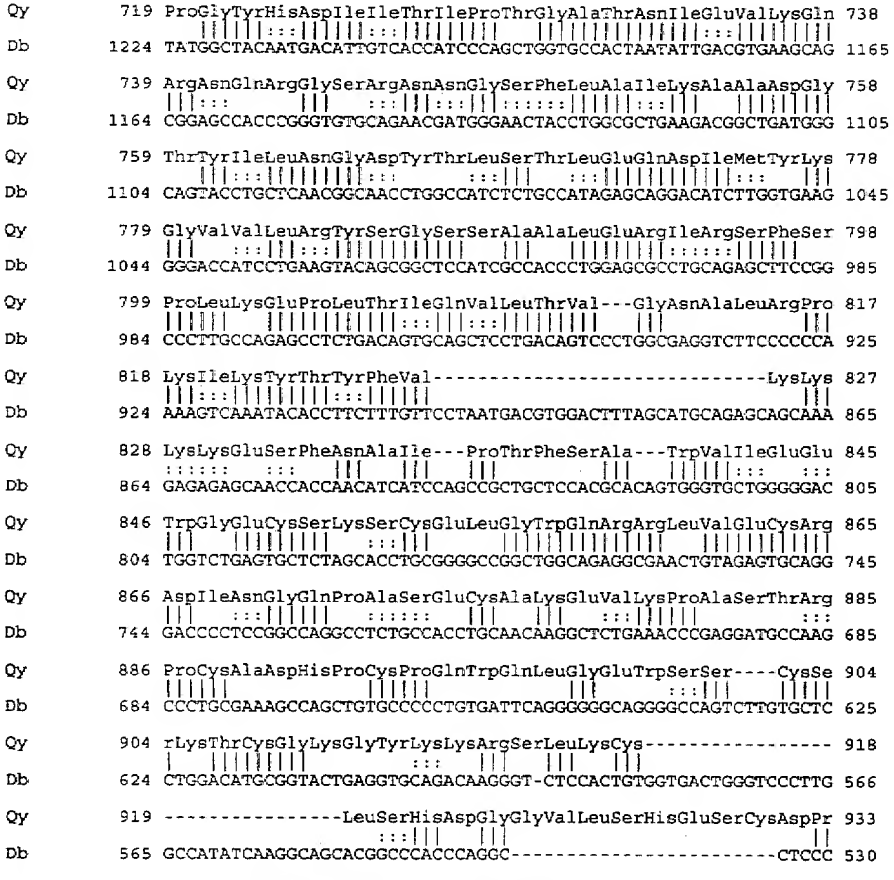
RESULT 8
US-09-392-184-7/c
; Sequence 7, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 3126
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3126)
; OTHER INFORMATION: reprolysin (ADAM family of metalloprotease)
US-09-392-184-7

Alignment Scores:

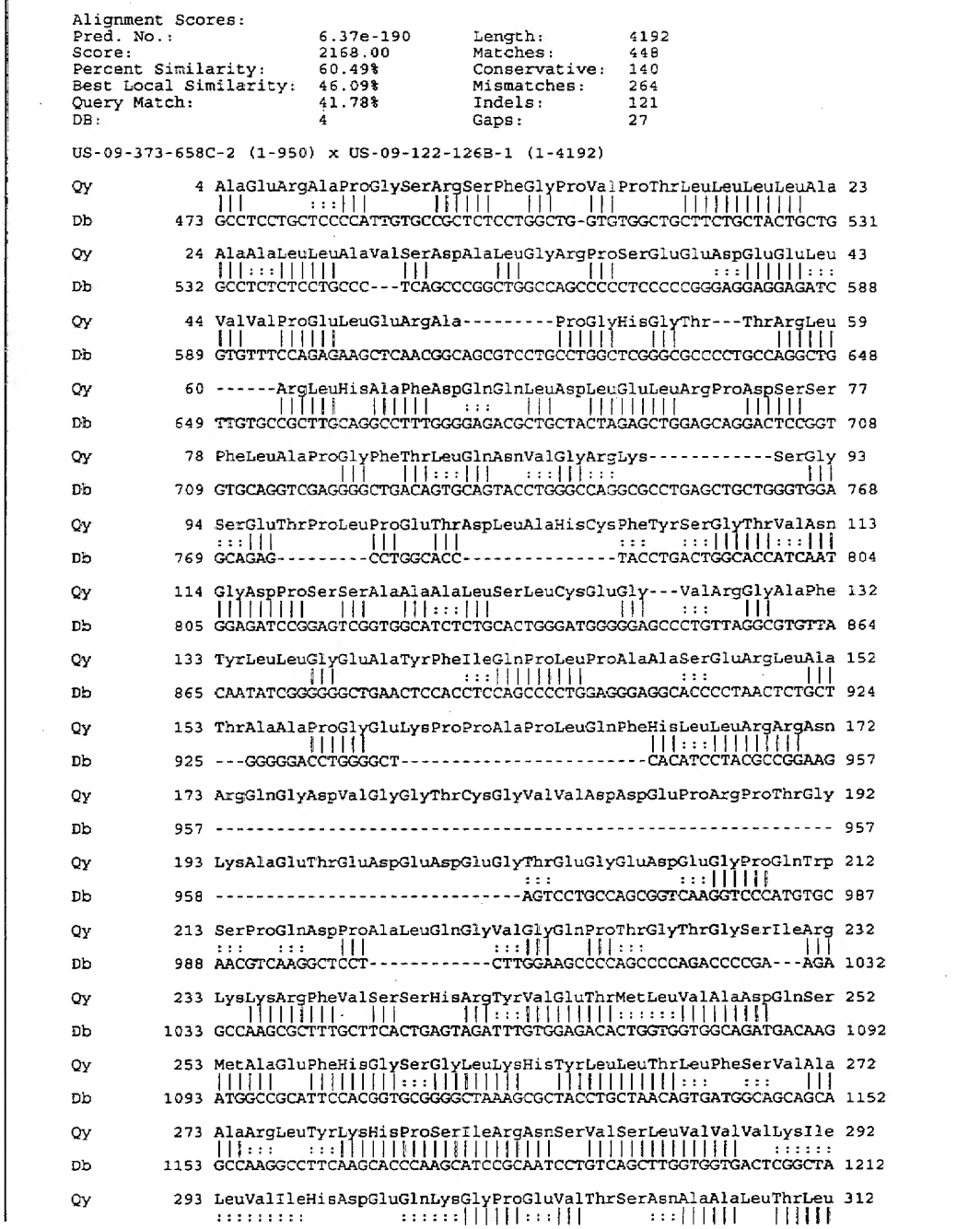
Pred. No.:	6.42e-191	Length:	3126
Score:	2176.50	Matches:	445
Percent Similarity:	62.46%	Conservative:	139
Best Local Similarity:	47.59%	Mismatches:	243
Query Match:	41.94%	Indels:	110
DB:	4	Gaps:	23

US-09-373-658C-2 (1-950) x US-09-392-184-7 (1-3126)





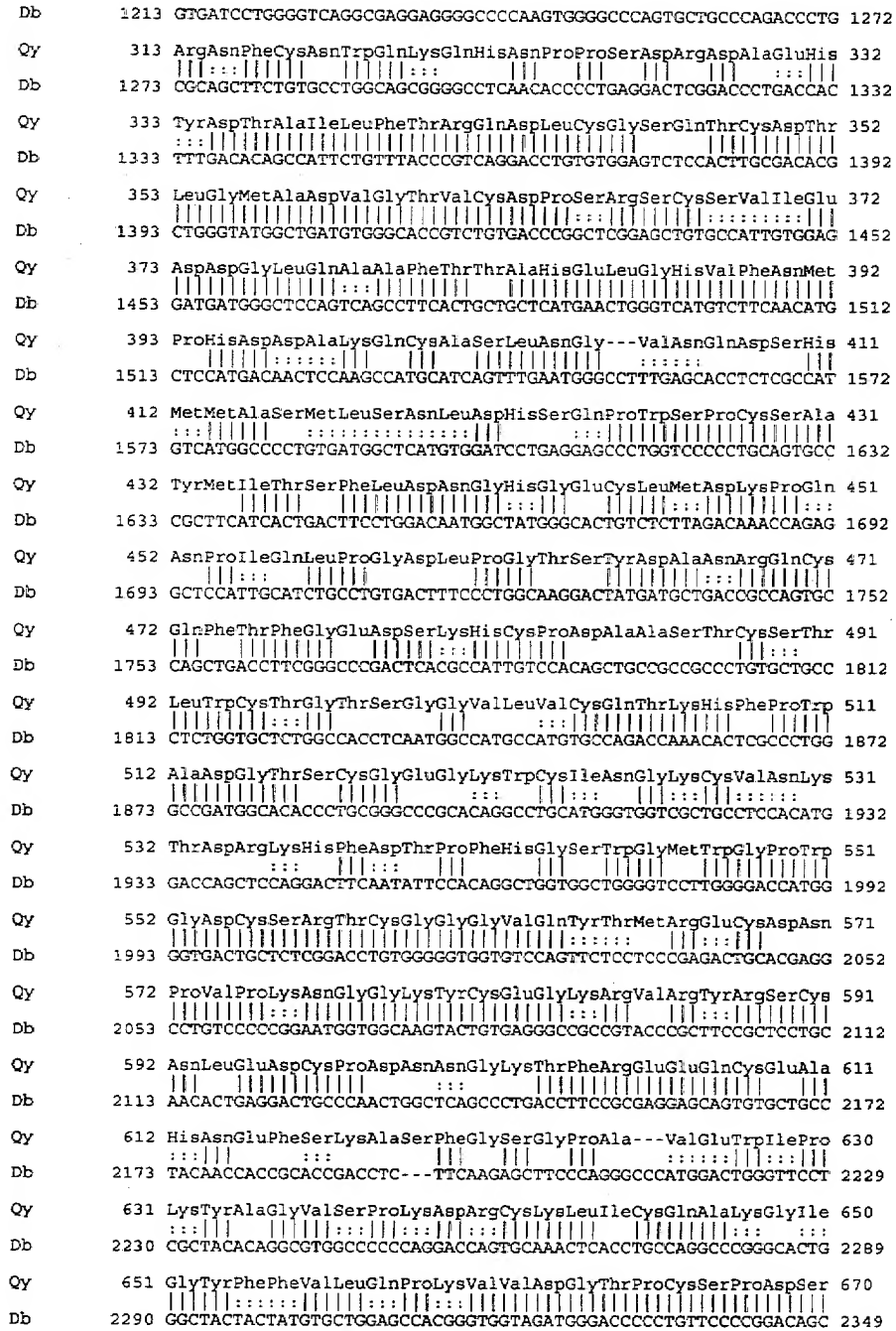
RESULT 9
US-09-122-126B-1
; Sequence 1, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-122-126B-1



Alignment Scores:

Pred. No.:	6.37e-190	Length:	4192
Score:	2168.00	Matches:	448
Percent Similarity:	60.49%	Conservative:	140
Best Local Similarity:	46.09%	Mismatches:	264
Query Match:	41.78%	Indels:	121
DB:	4	Gaps:	27

US-09-373-658C-2 (1-950) x US-09-122-126B-1 (1-4192)



RESULT 10
US-09-634-286A-1
; Sequence 1, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0

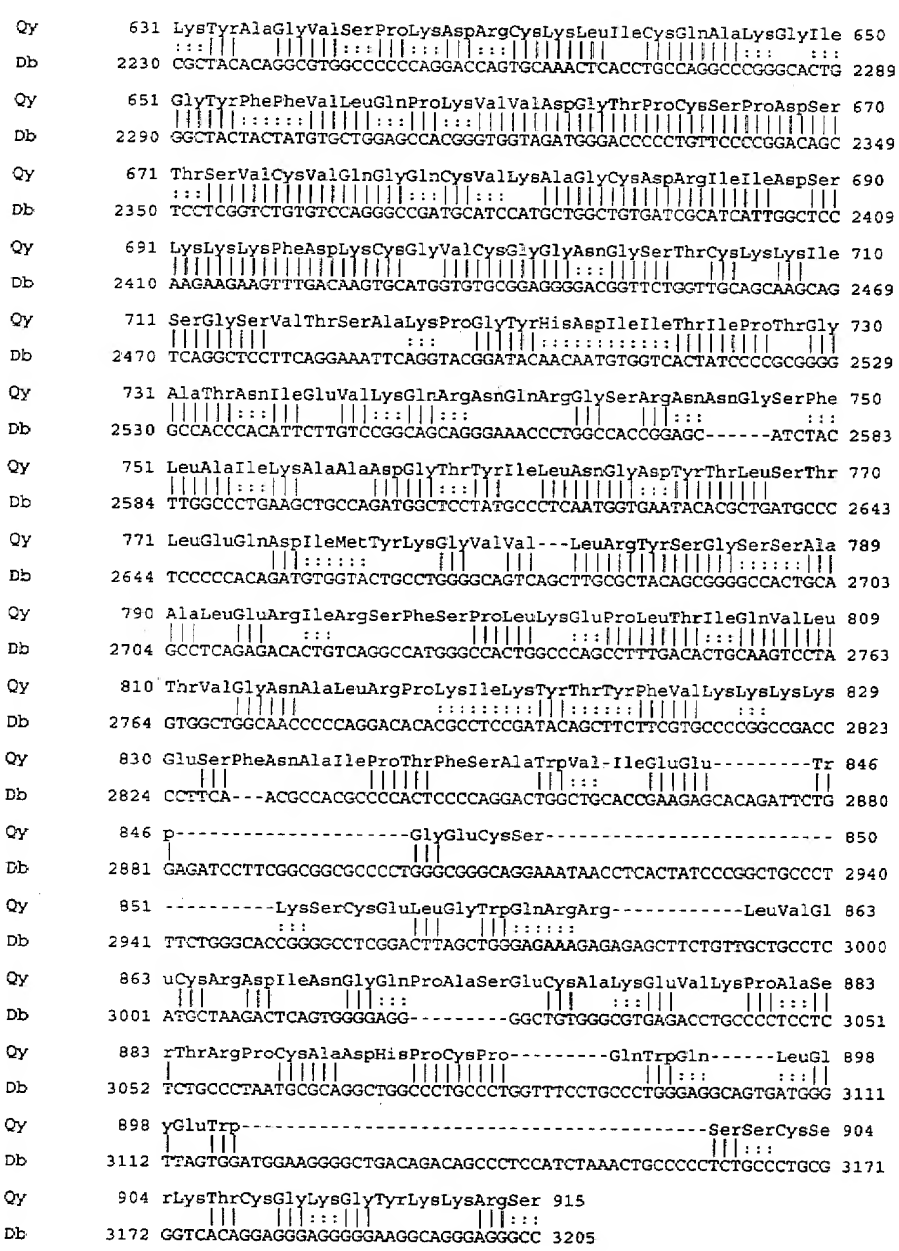
; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-634-286A-1

Alignment Scores:

Pred. No.:	6.37e-190	Length:	4192
Score:	2168.00	Matches:	448
Percent Similarity:	60.49%	Conservative:	140
Best Local Similarity:	46.09%	Mismatches:	264
Query Match:	41.78%	Indels:	121
DB:	4	Gaps:	27

US-09-373-658C-2 (1-950) x US-09-634-286A-1 (1-4192)

```
Qy          4 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla  23
              |||       :::|||       ||||||   |||   |||       ||||||||||||
Db        473 GCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTG-GTGTGGCTGCTTCTGCTACTGCTG 531

Qy         24 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu  43
              |||:::||||||       |||       |||       |||          :::|||||:::
Db        532 GCCTCTCTCCTGCCC---TCAGCCCGGCTGGCCAGCCCCCTCCCCCGGGAGGAGGAGATC 588

Qy         44 ValValProGluLeuGluArgAla---------ProGlyHisGlyThr---ThrArgLeu  59
              |||   ||||||                   ||||||   |||       ||||||
Db        589 GTGTTTCCAGAGAAGCTCAACGGCAGCGTCCTGCCTGGCTCGGGCGCCCCTGCCAGGCTG 648

Qy         60 ------ArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSer  77
                    ||||||   ||||||   :::   |||   |||||||||       ||||||
Db        649 TTGTGCCGCTTGCAGGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGT 708

Qy         78 PheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLys-----------SerGly  93
                  |||   |||:::|||   :::|||:::                        |||
Db        709 GTGCAGGTCGAGGGGCTGACAGTGCAGTACCTGGGCCAGGCGCCTGAGCTGCTGGGTGGA 768

Qy         94 SerGluThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsn 113
              :::|||         |||   |||                 :::   :::|||||:::|||
Db        769 GCAGAG---------CCTGGCACC---------------TACCTGACTGGCACCATCAAT 804

Qy        114 GlyAspProSerSerAlaAlaAlaLeuSerLeuCysGluGly---ValArgGlyAlaPhe 132
              |||||||||   |||   |||:::|||           |||   :::   |||
Db        805 GGAGATCCGGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTTA 864

Qy        133 TyrLeuLeuGlyGluAlaTyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAla 152
                  |||           :::|||||||||         :::           |||
Db        865 CAATATCGGGGGGCTGAACTCCACCTCCAGCCCCTGGAGGGAGGCACCCCTAACTCTGCT 924

Qy        153 ThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172
                  ||||||                        |||:::|||||||||
Db        925 ---GGGGGACCTGGGGCT-----------------------CACATCCTACGCCGGAAG 957

Qy        173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192

Db        957 ------------------------------------------------------------ 957

Qy        193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212
                                        :::         :::||||||
Db        958 ----------------------------AGTCCTGCCAGCGGTCAAGGTCCCATGTGC 987

Qy        213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232
              :::   :::   |||           :::|||   |||:::                |||
Db        988 AACGTCAAGGCTCCT-----------CTTGGAAGCCCCAGCCCCAGACCCCGA---AGA 1032

Qy        233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252
                 ||||||||||   |||       |||:::||||||||||:::::|||||||||
Db       1033 GCCAAGCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAG 1092

Qy        253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272
              ||||||   |||||||||:::|||||||||   ||||||||||||:::   :::   |||

Db       1093 ATGGCCGCATTCCACGGTGCGGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCA 1152

Qy        273 AlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIle 292
              |||:::   :::|||||||||||||||||||||||   ||||||||||||||   ::::::
Db       1153 GCCAAGGCCTTCAAGCACCCAAGCATCCGCAATCCTGTCAGCTTGGTGGTGACTCGGCTA 1212

Qy        293 LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeu 312
              :::::::::         ::::::|||||:::|||       :::||||||   ||||||
Db       1213 GTGATCCTGGGGTCAGGCGAGGAGGGGCCCCAAGTGGGGCCCAGTGCTGCCCAGACCCTG 1272

Qy        313 ArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis 332
              |||:::||||||   ||||||:::       |||   |||   |||   |||   :::|||
Db       1273 CGCAGCTTCTGTGCCTGGCAGCGGGGCCTCAACACCCCTGAGGACTCGGACCCTGACCAC 1332

Qy        333 TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThr 352
              :::||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db       1333 TTTGACACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCGACACG 1392

Qy        353 LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu 372
              ||||||||||||||||||||||||||||||||||||:::|||||||||:::::::|||
Db       1393 CTGGGTATGGCTGATGTGGGCACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAG 1452

Qy        373 AspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMet 392
              |||||||||||||||:::|||||||||   ||||||||||||||||||||||||||||||
Db       1453 GATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCATGAACTGGGTCATGTCTTCAACATG 1512

Qy        393 ProHisAspAspAlaLysGlnCysAlaSerLeuAsnGly---ValAsnGlnAspSerHis 411
              |||||:::::|||   |||   ||||||||||||   :::::           |||
Db       1513 CTCCATGACAACTCCAAGCCATGCATCAGTTTGAATGGGCCTTTGAGCACCTCTCGCCAT 1572

Qy        412 MetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAla 431
              :::|||||   :::::::::::::::|||      :::|||||||||||||||||||||
Db       1573 GTCATGGCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCC 1632

Qy        432 TyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGln 451
                  ||||||   ||||||||||||||||:::|||   ||||||:::|||||||||:::
Db       1633 CGCTTCATCACTGACTTCCTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAG 1692

Qy        452 AsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCys 471
                 |||:::   ||||||          ||||||   |||||||||:::||||||||||
Db       1693 GCTCCATTGCATCTGCCTGTGACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGC 1752

Qy        472 GlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThr 491
              |||   |||||||||   ||||||:::||||||||                  |||:::
Db       1753 CAGCTGACCTTCGGGCCCGACTCACGCCATTGTCCACAGCTGCCGCCGCCCTGTGCTGCC 1812

Qy        492 LeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProProTrp 511
              ||||||||:::|||       |||       :::|||||||||||||||   ||||||
Db       1813 CTCTGGTGCTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACACTCGCCCTGG 1872

Qy        512 AlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLys 531
              ||||||||||||   ||||||      :::   |||:::   |||:::|||::::::
Db       1873 GCCGATGGCACACCCTGCGGGCCCGCACAGGCCTGCATGGGTGGTCGCTGCCTCCACATG 1932

Qy        532 ThrAspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrp 551
                    :::   |||:::   |||       |||   ||||||   ||||||||||||
Db       1933 GACCAGCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCCTTGGGGACCATGG 1992

Qy        552 GlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsn 571
              |||||||||||||||||||||||||||||||||||||||||||::::::   |||:::|||
Db       1993 GGTGACTGCTCTCGGACCTGTGGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGG 2052

Qy        572 ProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCys 591
              |||||||||:::|||||||||||||||||||||||||:::|||   |||:::||||||||
Db       2053 CCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGGCCGCCGTACCCGCTTCCGCTCCTGC 2112

Qy        592 AsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAla 611
              |||   ||||||||||||       :::       ||||||||||||||||||||   |||
Db       2113 AACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCAGTGTGCTGCC 2172

Qy        612 HisAsnGluPheSerLysAlaSerPheGlySerGlyProAla---ValGluTrpIlePro 630
              :::|||      :::          |||   |||   |||      ::::::|||:::|||
Db       2173 TACAACCACCGCACCGACCTC---TTCAAGAGCTTCCCAGGGCCCATGGACTGGGTTCCT 2229
```



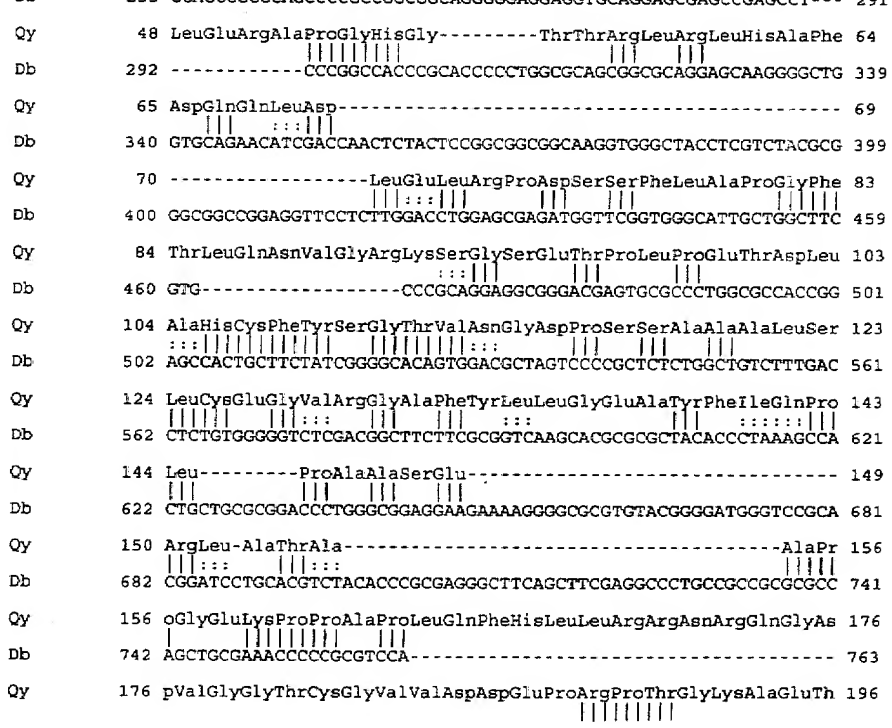
RESULT 11
US-09-122-126B-14
; Sequence 14, Application US/09122126B
; Patent No. 6451575

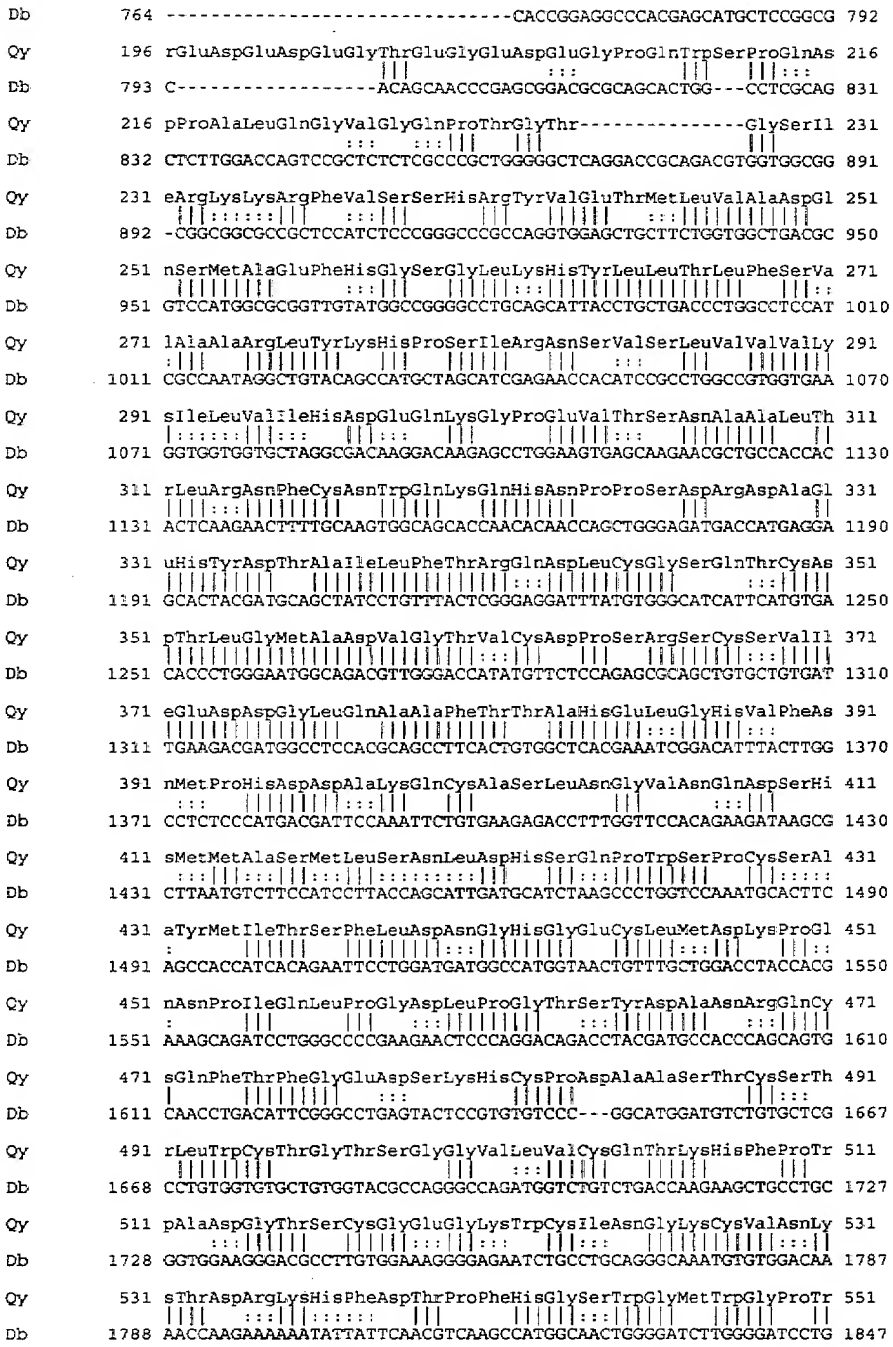
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-122-126B-14

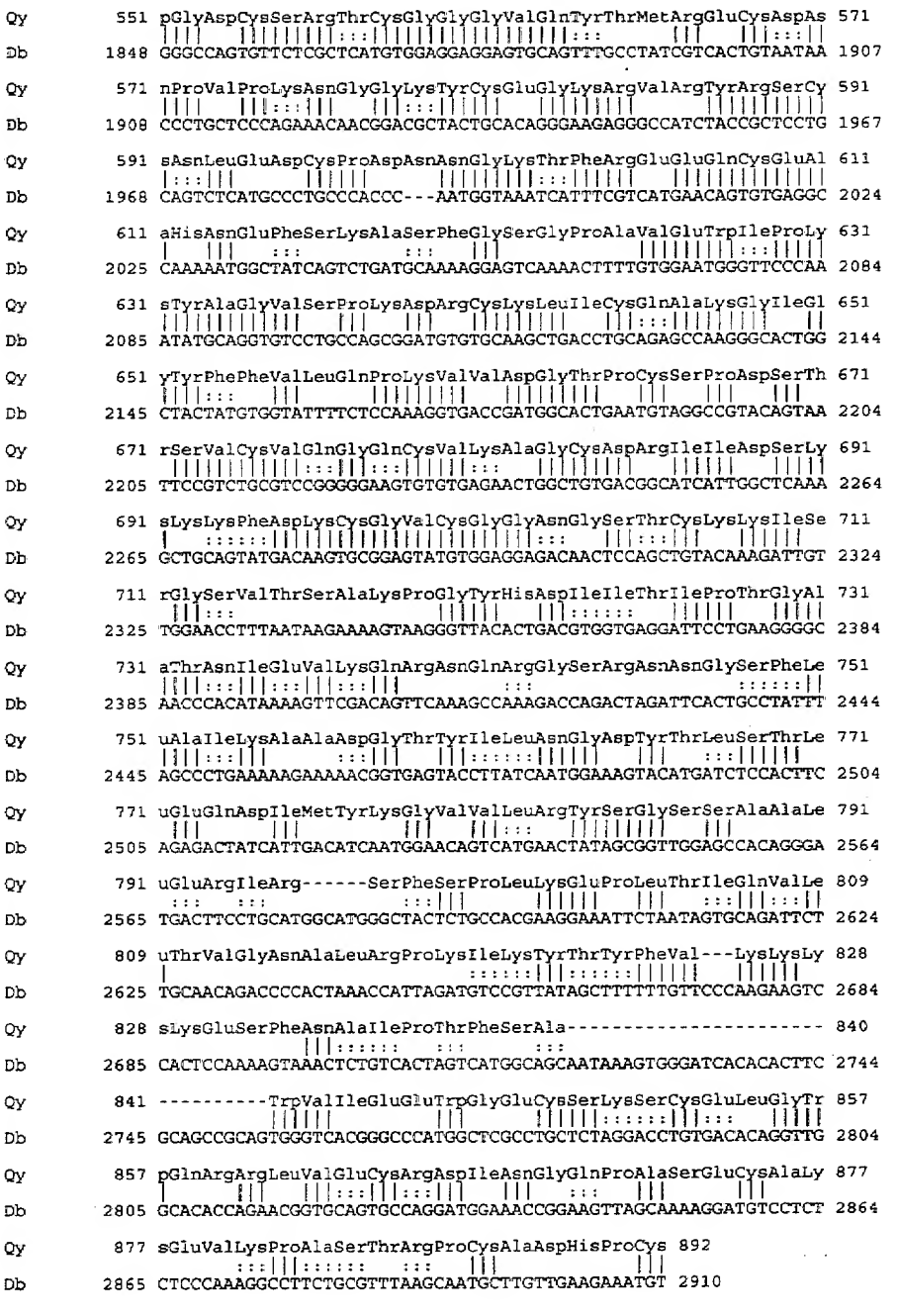
Alignment Scores:

Pred. No.:	3.49e-168	Length:	3250
Score:	1931.00	Matches:	395
Percent Similarity:	54.29%	Conservative:	124
Best Local Similarity:	41.32%	Mismatches:	316
Query Match:	37.21%	Indels:	122
DB:	4	Gaps:	17

US-09-373-658C-2 (1-950) x US-09-122-126B-14 (1-3250)







RESULT 12
US-09-634-286A-14
; Sequence 14, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-634-286A-14

Alignment Scores:

Pred. No.:	3.49e-168	Length:	3250
Score:	1931.00	Matches:	395
Percent Similarity:	54.29%	Conservative:	124
Best Local Similarity:	41.32%	Mismatches:	316
Query Match:	37.21%	Indels:	122
DB:	4	Gaps:	17

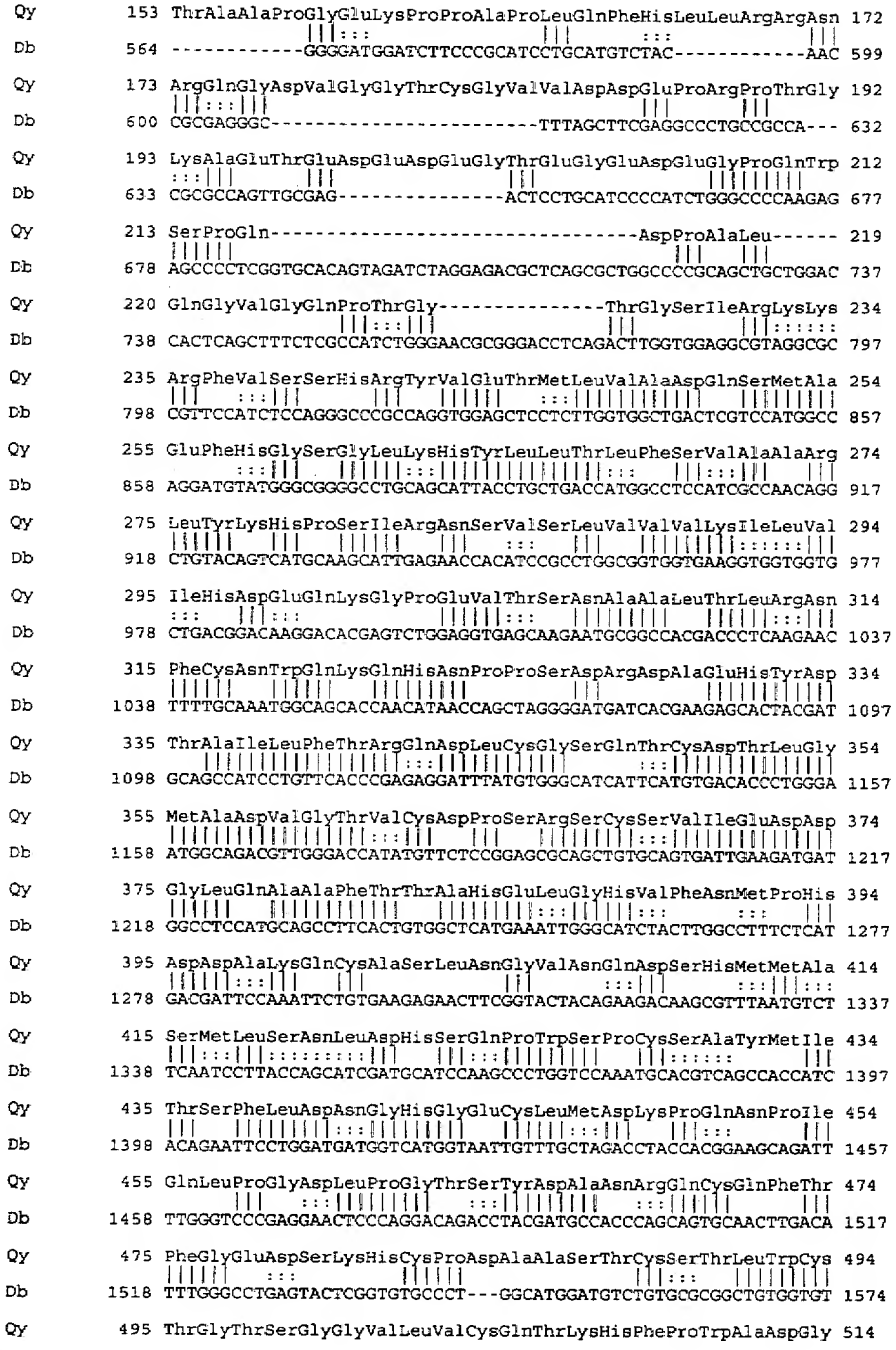
US-09-373-658C-2 (1-950) x US-09-634-286A-14 (1-3250)

```
Qy          8 ProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAlaAlaAlaLeuLeu 27
              |||                 |||     ||||||
Db        196 CCTGCCCAGGATAAAGCCGGGCAGCCTCCGACT--------------------GCTGCA 234

Qy         28 AlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeuValValProGlu 47
              |||   :::          |||      ||||||  :::|||         |||
Db        235 GCAGCCGCCCAGCCCCGCCGGCGGCAGGGGGAGGAGGTGCAGGAGCGAGCCGAGCCT--- 291

Qy         48 LeuGluArgAlaProGlyHisGly---------ThrThrArgLeuArgLeuHisAlaPhe 64
                       |||||||||                 |||   |||
Db        292 ------------CCCGGCCACCCGCACCCCCTGGCGCAGCGGCGCAGGAGCAAGGGGCTG 339

Qy         65 AspGlnGlnLeuAsp------------------------------------------- 69
                ||| :::|||
Db        340 GTGCAGAACATCGACCAACTCTACTCCGGCGGCGGCAAGGTGGGCTACCTCGTCTACGCG 399

Qy         70 ------------------LeuGluLeuArgProAspSerSerPheLeuAlaProGlyPhe 83
                           |||:::|||     |||  |||             ||||||
Db        400 GGCGGCCGGAGGTTCCTCTTGGACCTGGAGCGAGATGGTTCGGTGGGCATTGCTGGCTTC 459

Qy         84 ThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGluThrAspLeu 103
                                 :::|||      |||      |||
Db        460 GTG------------------CCCGCAGGAGGCGGGACGAGTGCGCCCTGGCGCCACCGG 501

Qy        104 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 123
              :::|||||||||||||   |||||||||:::      |||  |||  |||
Db        502 AGCCACTGCTTCTATCGGGGCACAGTGGACGCTAGTCCCCGCTCTCTGGCTGTCTTTGAC 561

Qy        124 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 143
              ||||||  |||:::  |||  |||  :::           |||  ::::::|||
Db        562 CTCTGTGGGGGTCTCGACGGCTTCTTCGCGGTCAAGCACGCGCGCTACACCCTAAAGCCA 621

Qy        144 Leu---------ProAlaAlaSerGlu------------------------------- 149
              |||         |||  |||  |||
Db        622 CTGCTGCGCGGACCCTGGGCGGAGGAAGAAAAGGGGCGCGTGTACGGGGATGGGTCCGCA 681

Qy        150 ArgLeu-AlaThrAla-------------------------------------AlaPr 156
              |||:::   |||:::                                     |||||
Db        682 CGGATCCTGCACGTCTACACCCGCGAGGGCTTCAGCTTCGAGGCCCTGCCGCCGCGCGCC 741

Qy        156 oGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAs 176
              |     |||||||||   |||
```

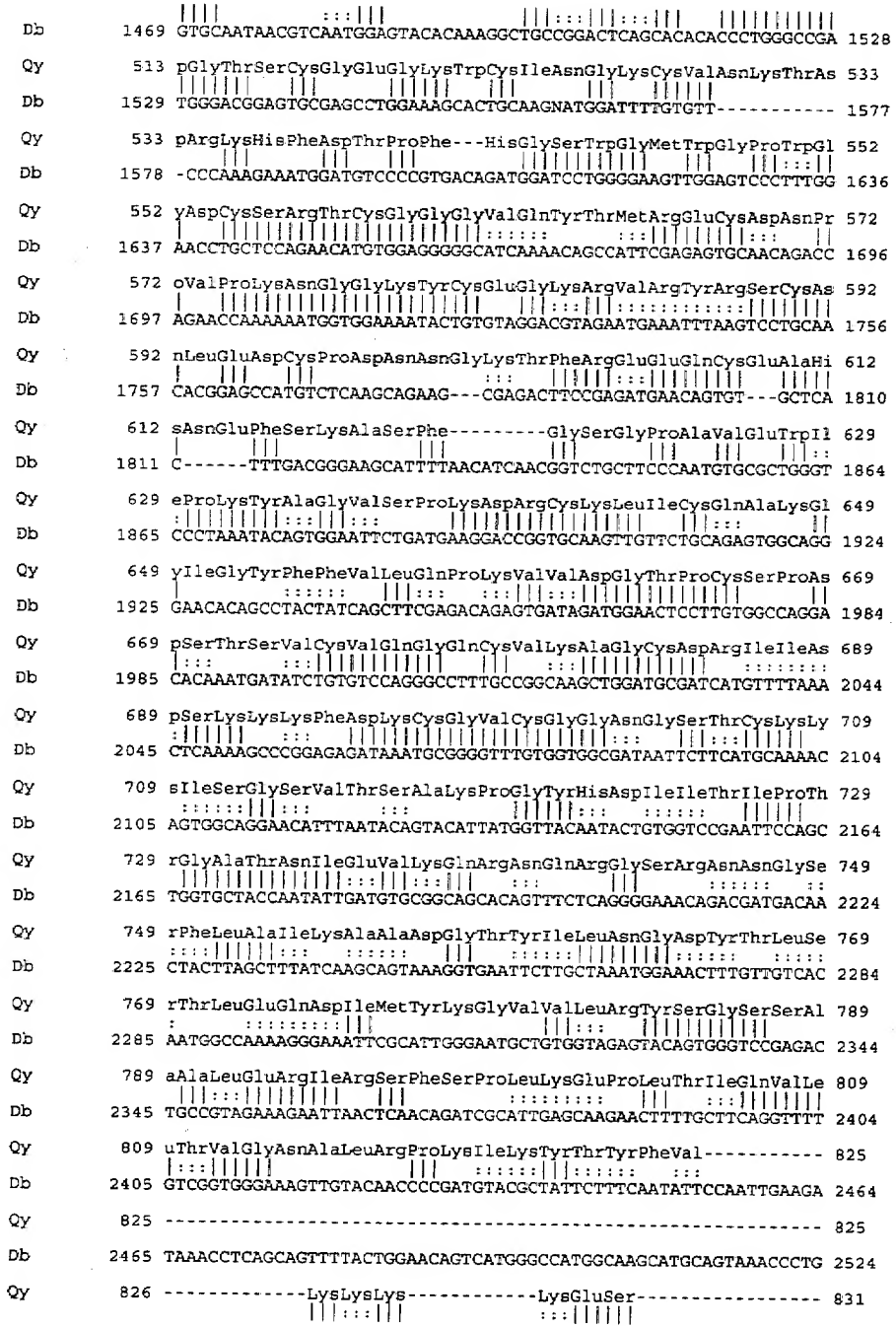
```
Db        742 AGCTGCGAAACCCCCGCGTCCA------------------------------------ 763

Qy        176 pValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluTh 196
                                                  |||||||||
Db        764 -----------------------------CACCGGAGGCCCACGAGCATGCTCCGGCG 792

Qy        196 rGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAs 216
                                  |||            :::          |||   |||:::
Db        793 C------------------ACAGCAACCCGAGCGGACGCGCAGCACTGG---CCTCGCAG 831

Qy        216 pProAlaLeuGlnGlyValGlyGlnProThrGlyThr---------------GlySerIl 231
                                  :::   :::|||   |||                  |||
Db        832 CTCTTGGACCAGTCCGCTCTCTCGCCCGCTGGGGGCTCAGGACCGCAGACGTGGTGGCGG 891

Qy        231 eArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGl 251
              |||::::::|||   :::|||      |||  ||||||  :::|||||||||||||
Db        892 -CGGCGGCGCCGCTCCATCTCCCGGGCCCGCCAGGTGGAGCTGCTTCTGGTGGCTGACGC 950

Qy        251 nSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerVa 271
              |||||||||      :::|||  ||||||:::|||||||||||||||||||  |||::
Db        951 GTCCATGGCGCGGTTGTATGGCCGGGGCCTGCAGCATTACCTGCTGACCCTGGCCTCCAT 1010

Qy        271 lAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLy 291
              :|||  |||||||||  |||  ||||||  |||  :::  |||  |||||||||
Db       1011 CGCCAATAGGCTGTACAGCCATGCTAGCATCGAGAACCACATCCGCCTGGCCGTGGTGAA 1070

Qy        291 sIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuTh 311
              |:::::|||:::  |||:::  |||      ||||||:::  |||||||||  ||
Db       1071 GGTGGTGGTGCTAGGCGACAAGGACAAGAGCCTGGAAGTGAGCAAGAACGCTGCCACCAC 1130

Qy        311 rLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGl 331
              ||||:::|||||||||  ||||||  |||||||||  |||  |||  ||
Db       1131 ACTCAAGAACTTTTGCAAGTGGCAGCACCAACACAACCAGCTGGGAGATGACCATGAGGA 1190

Qy        331 uHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAs 351
              ||||||||||  ||||||||||||||||||:::||||||||||||  :::||||||
Db       1191 GCACTACGATGCAGCTATCCTGTTTACTCGGGAGGATTTATGTGGGCATCATTCATGTGA 1250

Qy        351 pThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIl 371
              |||||||||||||||||||||||||||:::|||  |||  |||||||||:::|||||
Db       1251 CACCCTGGGAATGGCAGACGTTGGGACCATATGTTCTCCAGAGCGCAGCTGTGCTGTGAT 1310

Qy        371 eGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAs 391
              ||||||||||||||||  ||||||||||||  ||||||||||:::|||||:::
Db       1311 TGAAGACGATGGCCTCCACGCAGCCTTCACTGTGGCTCACGAAATCGGACATTTACTTGG 1370

Qy        391 nMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHi 411
              :::  ||||||||||:::|||  |||              |||      :::|||
Db       1371 CCTCTCCCATGACGATTCCAAATTCTGTGAAGAGACCTTTGGTTCCACAGAAGATAAGCG 1430

Qy        411 sMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAl 431
              :::|||:::|||:::|||:::::::::|||  |||:::|||||||||  |||:::::
Db       1431 CTTAATGTCTTCCATCCTTACCAGCATTGATGCATCTAAGCCCTGGTCCAAATGCACTTC 1490

Qy        431 aTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGl 451
              :  ||||||  |||||||||:::|||||||||  ||||||:::|||  |||::
Db       1491 AGCCACCATCACAGAATTCCTGGATGATGGCCATGGTAACTGTTTGCTGGACCTACCACG 1550

Qy        451 nAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCy 471
              :    |||      |||  :::|||||||||  :::|||||||||  :::|||||
Db       1551 AAAGCAGATCCTGGGCCCCGAAGAACTCCCAGGACAGACCTACGATGCCACCCAGCAGTG 1610

Qy        471 sGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerTh 491
              |      |||||||||  :::      ||||||          |||:::
Db       1611 CAACCTGACATTCGGGCCTGAGTACTCCGTGTGTCCC---GGCATGGATGTCTGTGCTCG 1667

Qy        491 rLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTr 511
              |||||||||          |||  :::||||||  ||||||      |||
Db       1668 CCTGTGGTGTGCTGTGGTACGCCAGGGCCAGATGGTCTGTCTGACCAAGAAGCTGCCTGC 1727

Qy        511 pAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLy 531
              :::||||||  ||||||:::|||:::  ||||:::  ||||||||||||:::||
Db       1728 GGTGGAAGGGACGCCTTGTGGAAAGGGGAGAATCTGCCTGCAGGGCAAATGTGTGGACAA 1787
```

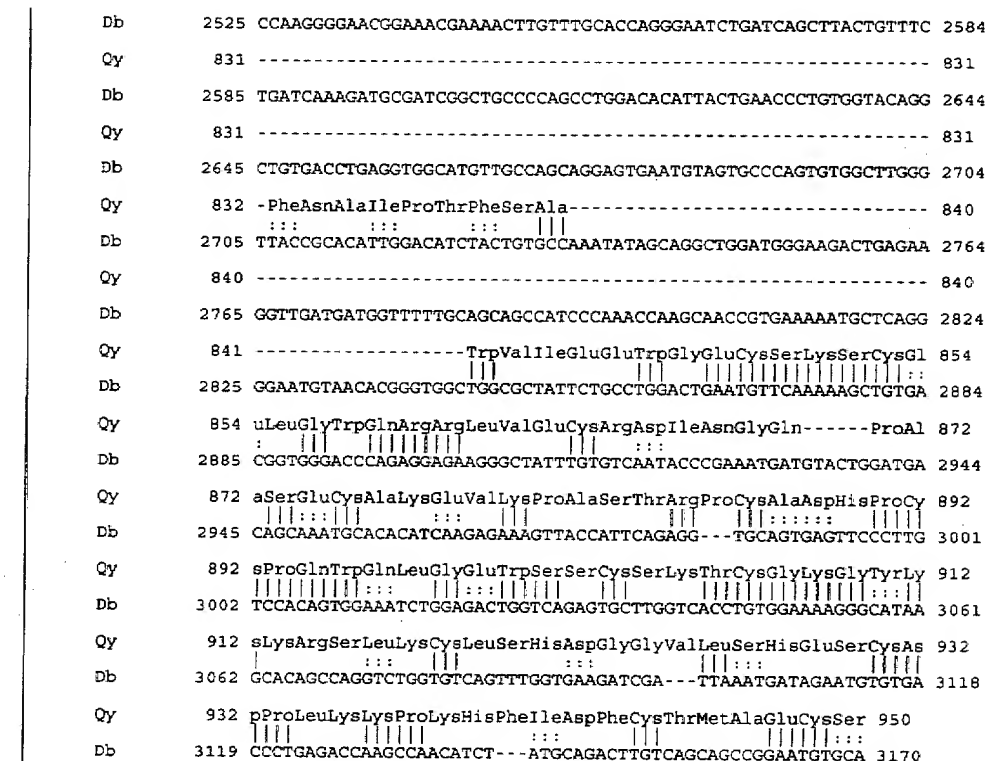
```
Qy        531 sThrAspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTr 551
Db       1788 AACCAAGAAAAAATATTATTCAACGTCAAGCCATGGCAACTGGGGATCTTGGGGATCCTG 1847

Qy        551 pGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAs 571
Db       1848 GGGCCAGTGTTCTCGCTCATGTGGAGGAGGAGTGCAGTTTGCCTATCGTCACTGTAATAA 1907

Qy        571 nProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCy 591
Db       1908 CCCTGCTCCCAGAAACAACGGACGCTACTGCACAGGGAAGAGGGCCATCTACCGCTCCTG 1967

Qy        591 sAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAl 611
Db       1968 CAGTCTCATGCCCTGCCCACCC---AATGGTAAATCATTTCGTCATGAACAGTGTGAGGC 2024

Qy        611 aHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLy 631
Db       2025 CAAAAATGGCTATCAGTCTGATGCAAAAGGAGTCAAAACTTTGTGGAATGGGTTCCCAA 2084

Qy        631 sTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGl 651
Db       2085 ATATGCAGGTGTCCTGCCAGCGGATGTGTGCAAGCTGACCTGCAGAGCCAAGGGCACTGG 2144

Qy        651 yTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerTh 671
Db       2145 CTACTATGTGGTATTTTCTCCAAAGGTGACCGATGGCACTGAATGTAGGCCGTACAGTAA 2204

Qy        671 rSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLy 691
Db       2205 TTCCGTCTGCGTCCGGGGGAAGTGTGTGAGAACTGGCTGTGACGGCATCATTGGCTCAAA 2264

Qy        691 sLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSe 711
Db       2265 GCTGCAGTATGACAAGTGCGGAGTATGTGGAGGAGACAACTCCAGCTGTACAAAGATTGT 2324

Qy        711 rGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAl 731
Db       2325 TGGAACCTTTAATAAGAAAAGTAAGGGTTACACTGACGTGGTGAGGATTCCTGAAGGGGC 2384

Qy        731 aThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLe 751
Db       2385 AACCCACATAAAAGTTCGACAGTTCAAAGCCAAAGACCAGACTAGATTCACTGCCTATTT 2444

Qy        751 uAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLe 771
Db       2445 AGCCCTGAAAAAGAAAAACGGTGAGTACCTTATCAATGGAAAGTACATGATCTCCACTTC 2504

Qy        771 uGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLe 791
Db       2505 AGAGACTATCATTGACATCAATGGAACAGTCATGAACTATAGCGGTTGGAGCCACAGGGA 2564

Qy        791 uGluArgIleArg------SerPheSerProLeuLysGluProLeuThrIleGlnValLe 809
Db       2565 TGACTTCCTGCATGGCATGGGCTACTCTGCCACGAAGGAAATTCTAATAGTGCAGATTCT 2624

Qy        809 uThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheVal---LysLysLy 828
Db       2625 TGCAACAGACCCCACTAAACCATTAGATGTCCGTTATAGCTTTTTTGTTCCCAAGAAGTC 2684

Qy        828 sLysGluSerPheAsnAlaIleProThrPheSerAla---------------------- 840
Db       2685 CACTCCAAAAGTAAACTCTGTCACTAGTCATGGCAGCAATAAAGTGGGATCACACACTTC 2744

Qy        841 ----------TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTr 857
Db       2745 GCAGCCGCAGTGGGTCACGGGCCCATGGCTCGCCTGCTCTAGGACCTGTGACACAGGTTG 2804

Qy        857 pGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLy 877
Db       2805 GCACACCAGAACGGTGCAGTGCCAGGATGGAAACCGGAAGTTAGCAAAAGGATGTCCTCT 2864

Qy        877 sGluValLysProAlaSerThrArgProCysAlaAspHisProCys 892
Db       2865 CTCCCAAAGGCCTTCTGCGTTTAAGCAATGCTTGTTGAAGAAATGT 2910
```

```
RESULT 13
US-09-369-364A-1
; Sequence 1, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
;  APPLICANT:  Apte, Suneel
;  APPLICANT:  Hurskainen, Tiina L.
;  APPLICANT:  Hirohata, Satoshi
;  TITLE OF INVENTION:  Nucleic Acids Encoding Zinc Metalloproteases
;  FILE REFERENCE:  26473/4007/10-30-00
;  CURRENT APPLICATION NUMBER: US/09/369,364A
;  CURRENT FILING DATE:  1999-08-06
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3002
;   TYPE: DNA
;   ORGANISM: mus musculus ADAMTS-5
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (18)..(2810)
US-09-369-364A-1

Alignment Scores:
Pred. No.:                4.88e-167      Length:          3002
Score:                    1918.00        Matches:         407
Percent Similarity:       54.79%         Conservative:    136
Best Local Similarity:    41.07%         Mismatches:      321
Query Match:              36.96%         Indels:          128
DB:                       4              Gaps:            23

US-09-373-658C-2 (1-950) x US-09-369-364A-1 (1-3002)

Qy         19 LeuLeuLeuLeuAlaAlaAlaLeuLeuAlaValSer---------------------- 30
Db         51 CTGCTGCTGCTGAGCGCGTCCTGCCTGTCCCTGGCCGCTGACAGCCCCGCCGCGGCACCT 110

Qy         31 ----------------------AspAlaLeuGlyArgProSerGluGluAspGluGlu 42
Db        111 GCCCAGGATAAAACCAGGCAGCCTCAGGCTGCAGCAGCGGCCGCCGAGCCGGACCAG--- 167

Qy         43 LeuValValProGluLeuGlu------ArgAlaProGlyHis---------------- 54
Db        168 ---------CCGCAGGGGGAGGAAACACGGGAGCGAGGCCATTTACAACCCTTGGCCGGG 218

Qy         55 ------------------------------------------------------GlyThr 56
Db        219 CAGCGCAGGAGCGGCGGGCTGGTCCATAATATAGACCAACTCTACTCTGGCGGTGGCAAA 278

Qy         57 ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSer 76
Db        279 GTGGGCTACCTTGTCTACGCGGGCGGCCGGAGGTTCCTGCTGGACCTGGAGAGAGATGAC 338

Qy         77 SerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThr 96
Db        339 ACAGTGGGTGCTGCTGGTAGCATCGTTACTGCAGGAGGAGGGCTGAGCGCATCC------ 392

Qy         97 ProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspPro 116
Db        393 ---------TCTGGCCACCGGGGTCACTGTTTCTACAGAGGCACCGTGGACGGCAGCCCT 443

Qy        117 SerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGly 136
Db        444 CGATCCCTAGCTGTCTTTGACCTCTGCGGGGGTCTCGATGGCTTCTTTGCAGTCAAGCAT 503

Qy        137 GluAlaTyrPheIleGlnProLeuProAlaAlaSer------------GluArgLeuAla 152
Db        504 GCGCGCTACACTCTAAAGCCACTCCTGCGTGGGTCCTGGGCAGAGTATGAACGAATTTAT 563
```


Qy 153 ThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172
Db 564 ----------GGGGATGGATCTTCCCGCATCCTGCATGTCTAC----------AAC 599
Qy 173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192
Db 600 CGCGAGGGC----------TTTAGCTTCGAGGCCCTGCCGCCA--- 632
Qy 193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212
Db 633 CGCGCCAGTTGCGAG----------ACTCCTGCATCCCCATCTGGGCCCCAAGAG 677
Qy 213 SerProGln----------AspProAlaLeu------ 219
Db 678 AGCCCCTCGGTGCACAGTAGATCTAGGAGACGCTCAGCGCTGGCCCCGCAGCTGCTGGAC 737
Qy 220 GlnGlyValGlyGlnProThrGly----------ThrGlySerIleArgLysLys 234
Db 738 CACTCAGCTTTCTCGCCATCTGGGAACGCGGGACCTCAGACTTGGTGGAGGCGTAGGCGC 797
Qy 235 ArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAla 254
Db 798 CGTTCCATCTCCAGGGCCCGCCAGGTGGAGCTCCTCTTGGTGGCTGACTCGTCCATGGCC 857
Qy 255 GluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArg 274
Db 858 AGGATGTATGGGCGGGGCCTGCAGCATTACCTGCTGACCATGGCCTCCATCGCCAACAGG 917
Qy 275 LeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuVal 294
Db 918 CTGTACAGTCATGCAAGCATTGAGAACCACATCCGCCTGGCGGTGGTGAAGGTGGTGGTG 977
Qy 295 IleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsn 314
Db 978 CTGACGGACAAGGACACGAGTCTGGAGGTGAGCAAGAATGCGGCCACGACCCTCAAGAAC 1037
Qy 315 PheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAsp 334
Db 1038 TTTTGCAAATGGCAGCACCAACATAACCAGCTAGGGGATGATCACGAAGAGCACTACGAT 1097
Qy 335 ThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGly 354
Db 1098 GCAGCCATCCTGTTCACCCGAGAGGATTTATGTGGGCATCATTCATGTGACACCCTGGGA 1157
Qy 355 MetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAsp 374
Db 1158 ATGGCAGACGTTGGGACCATATGTTCTCCGGAGCGCAGCTGTGCAGTGATTGAAGATGAT 1217
Qy 375 GlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHis 394
Db 1218 GGCCTCCATGCAGCCTTCACTGTGGCTCATGAAATTGGGCATCTACTTGGCCTTTCTCAT 1277
Qy 395 AspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAla 414
Db 1278 GACGATTCCAAATTCTGTGAAGAGAACTTCGGTACTACAGAAGACAAGCGTTTAATGTCT 1337
Qy 415 SerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMetIle 434
Db 1338 TCAATCCTTACCAGCATCGATGCATCCAAGCCCTGGTCCAAATGCACGTCAGCCACCATC 1397
Qy 435 ThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIle 454
Db 1398 ACAGAATTCCTGGATGATGGTCATGGTAATTGTTTGCTAGACCTACCACGGAAGCAGATT 1457
Qy 455 GlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThr 474
Db 1458 TTGGGTCCCGAGGAACTCCCAGGACAGACCTACGATGCCACCCAGCAGTGCAACTTGACA 1517
Qy 475 PheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCys 494
Db 1518 TTTGGGCCTGAGTACTCGGTGTGCCCT---GGCATGGATGTCTGTGCGCGGCTGTGGTGT 1574
Qy 495 ThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProProTrpAlaAspGly 514
Db 1575 GCTGTGGTGCGCCAAGGCCAAATGGTGTGTCTGACCAAGAAGCTGCCGGCTGTGGAGGGC 1634
Qy 515 ThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThrAspArg 534
Db 1635 ACTCCCTGTGGGAAGGGAAGAGTCTGCCTTCAAGGCAAATGTGTGGACAAAACTAAGAAA 1694
Qy 535 LysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCys 554
Db 1695 AAATATTACTCGACATCAAGCCATGGAAATTGGGGGTCCTGGGGCCCCTGGGGTCAGTGT 1754
Qy 555 SerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValPro 574
Db 1755 TCTCGCTCATGCGGGGGAGGAGTGCAGTTTGCCTACCGCCATTGTAATAACCCTGCACCT 1814
Qy 575 LysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGlu 594
Db 1815 CGAAACAGTGGCCGCTACTGCACAGGGAAGAGGGCCATATACCGTTCCTGCAGTGTTACA 1874
Qy 595 AspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGlu 614
Db 1875 CCCTGCCCACCC---AATGGTAAATCTTTTCGCCATGAGCAGTGTGAAGCCAAAAATGGC 1931
Qy 615 PheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGly 634
Db 1932 TATCAGTCTGATGCAAAAGGAGTCAAAACATTTGTAGAATGGGTTCCCAAATATGCAGGT 1991
Qy 635 ValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePhe 654
Db 1992 GTCCTGCCGGCAGATGTGTGCAAGCTTACCTGCAGAGCTAAGGGCACAGGCTACTATGTG 2051
Qy 655 ValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCys 674
Db 2052 GTCTTTTCTCCAAAGGTTACGGATGGGACTGAATGCAGGCCGTACAGCAACTCTGTGTGT 2111
Qy 675 ValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPhe 694
Db 2112 GTCCGAGGACGGTGTGTGAGAACTGGATGTGACGGCATTATTGGCTCAAAGCTACAATAT 2171
Qy 695 AspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerVal 714
Db 2172 GACAAGTGTGGAGTGTGCGGAGGGGATAACTCCAGTTGTACAAAGATTATCGGAACCTTC 2231
Qy 715 ThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIle 734
Db 2232 AATAAAAAAAAGCAAGGGTTATACTGACGTTGTGAGGATCCCTGAAGGAGCAACCCACATA 2291
Qy 735 GluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLys 754
Db 2292 AAAGTCCGACAGTTCAAAGCCAAAGACCAGACTAGATTCCCTGCCTACTTAGCCCTGAAG 2351
Qy 755 AlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAsp 774
Db 2352 AAGAAAACTGGCGAGTACCTTATCAATGGCAAGTACATGATTTCCACTTCAGAGACCATC 2411
Qy 775 IleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIle 794
Db 2412 ATCGACATCAATGGTACCGTCATGAACTACAGTGGATGGAGCCACAGAGATGATTTTTTA 2471
Qy 795 Arg------SerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGly 812
Db 2472 CATGGGATGGGCTATTCAGCCACAAAAGAAATCCTGATCGTGCAGATCCTTGCCACAGAC 2531
Qy 813 AsnAlaLeuArgProLysIleLysTyrThrTyrPheVal---LysLysLysLysGluSer 831
Db 2532 CCAACTAAAGCGCTAGGCGTCCGTTACAGCTTTTTGTTCCCAAGAAGACCACTCAAAAA 2591
Qy 832 PheAsnAlaIle----------ProThrPheSerAla 840
Db 2592 GTAAACTCTGTCATCAGCCATGGCAGCAACAAGGTGGGACCACACTCTACACAGCTGCAG 2651
Qy 841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860

```
Db       2652 TGGGTGACAGGTCCATGGCTGGCCTGCTCCAGGACCTGTGACACAGGCTGGCACACTAGG 2711

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880

Db       2712 ACCGTGCAGTGCCAGGATGGAAACAGGAAATTAGCTAAAGGATGCCTTCTCTCTCAGAGG 2771

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCys---ProGlnTrpGlnLeuGlyGlu 899

Db       2772 CCTTCTGCATTTAAGCAATGTCTGCTGAAGAAATGTTAGCCTGTG-----------GTT 2819

Qy        900 TrpSerSerCysSerLys-------------------------ThrCysGly------ 908

Db       2820 TACTCTAA-TGCACAAAAAAACAACAGGAGGATCATCGCAGATACAGCTGTGGTGAAGAC 2878

Qy        909 LysGlyTyrLysLysArgSerLeuLysCysLeu 919

Db       2879 AAGGCCTACCCAAAGCACAGAAAGTCATGCCTT 2911

RESULT 14
US-09-369-364A-12
; Sequence 12, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
;  APPLICANT:  Apte, Suneel
;  APPLICANT:  Hurskainen, Tiina L.
;  APPLICANT:  Hirohata, Satoshi
;  TITLE OF INVENTION:  Nucleic Acids Encoding Zinc Metalloproteases
;  FILE REFERENCE:  26473/4007/10-30-00
;  CURRENT APPLICATION NUMBER: US/09/369,364A
;  CURRENT FILING DATE:  1999-08-06
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 5804
;   TYPE: DNA
;   ORGANISM: Homo sapiens ADAMTS-9
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3)..(5648)
;   NAME/KEY: misc_feature
;   LOCATION: (1406)
;   OTHER INFORMATION: n=T
;   NAME/KEY: misc_feature
;   LOCATION: (1563)
;   OTHER INFORMATION: n=T
US-09-369-364A-12

Alignment Scores:
Pred. No.:                1.26e-151      Length:          5804
Score:                    1756.50        Matches:         368
Percent Similarity:       50.93%         Conservative:    151
Best Local Similarity:    36.11%         Mismatches:      308
Query Match:              33.85%         Indels:          193
DB:                       4              Gaps:            24

US-09-373-658C-2 (1-950) x US-09-369-364A-12 (1-5804)

Qy          60 ArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeu 79

Db         309 CGCCTCTCTGCCTTCGGCCAGCAGTTTCTATTTAATCTCACCGCCAATGCCGGATTTATC 368

Qy          80 AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeu--- 98

Db         369 GCTCCACTGTTCACTGTCACCCTCCTTGGGACGCCCGGGGTGAATCAGACCAAGTTTTAT 428

Qy          99 ------ProGluThrAspLeuAlaHisCysPheTyr-SerGlyThrValAsnGlyAspPr 116

Db         429 TCCGAAGAGGAAGCGGAACTAAAGCACTGTTTCTACAAAAGGCTATGTCAATACCAACTC 488

Qy         116 oSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGl 136

Db         489 CGAGCACACGGCCGTCATCAGCCTCTGCTCAGGAATG---------------------- 525

Qy         136 yGluAlaTyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaPr 156

Db         526 --------------------------------AACACAAAAATAGGCACAGTAAAGAC 551

Qy         156 oGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAs 176

Db         552 AAGAAGAAAACCAGA-GCAAGAAAATGGGGAGAA------AGGATTAACCTGGCTGGTGA 604

Qy         176 pValGlyGly---ThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGl 195

Db         605 CGTAGCAGCATTAAACAGCGGCTTAGCAACAGAGGCATTTTCTGCTTATGGTAATAAGAC 664

Qy         195 uThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGl 215

Db         665 GGACAACACAAGAGAAAAGAGGACCCACAGA---------------------------- 695

Qy         215 nAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysAr 235

Db         696 ------------------------------------------------AGGACAAAACG 706

Qy         235 gPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGl 255

Db         707 TTTTTTATCCTATCCACGGTTTGTAGAAGTCTTGGTGGTGGCAGACAACAGAATGGTTTC 766

Qy         255 uPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLe 275

Db         767 ATACCATGGAGAAAACCTTCAACACTATATTTTAACTTTAATGTCAATTGTAGCCTCTAT 826

Qy         275 uTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIl 295

Db         827 CTATAAAGACCCAAGTATTGGAAATTTAATTAATATTGTTATTGTGAACTTAATTGTGAT 886

Qy         295 eHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPh 315

Db         887 TCATAATGAACAGGATGGGCCTTCCATATCTTTAATGCTCAGACAACATTAAAAAACTT 946

Qy         315 eCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspTh 335

Db         947 TTGCCAGTGGCAGCATTCGAACAGTCCA-----------GGTGGAATCCATCATGATAC 994

Qy         335 rAlaIleLeuPheThrArgGlnAspLeuCys---GlySerGlnThrCysAspThrLeuGl 354

Db         995 TGCTGTTCTCTTAACAAGACAGGATATCTGCAGAGCTCACGACAAATGTGATACCTTAGG 1054

Qy         354 yMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAs 374

Db        1055 CCTGGCTGAACTGGGAACCATTTGTGATCCCTATAGAAGCTGTTCTATTAGTGAAGATAG 1114

Qy         374 pGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHi 394

Db        1115 TGGATTGAGTACAGCTTTTACGATCGCCCATGAGCTGGGCCATGTGTTTAACATGCCTCA 1174

Qy         394 sAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAl 414

Db        1175 TGATGACAACAACAAATGTAAAGAA---GAAGGAGTTAAGAGTCCCCAGCATGTCATGGC 1231

Qy         414 aSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMetIl 434

Db        1232 TCCAACACTGAACTTCTACACCAACCCCTGGATGTGGTCAAAGTGTAGTCGAAAATATAT 1291

Qy         434 eThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsn---Pr 453

Db        1292 CACTGAGTTTTTAGACACTGGTTATGGCGAGTGTTTGCTTAACGAACCTGAATCCAGACC 1351

Qy         453 oIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPh 473

Db        1352 CTACCCTTTGCCTGTCCAACTGCCAGGCATCCTTTACAACGTGAATAAACAATGNGAATT 1411

Qy         473 eThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTr 493

Db        1412 GATTTTTGGACCAGGTTCTCAGGTGTGCCCA---TATATGATGCAGTGCAGACGGCTCTG 1468

Qy         493 pCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAs 513
```



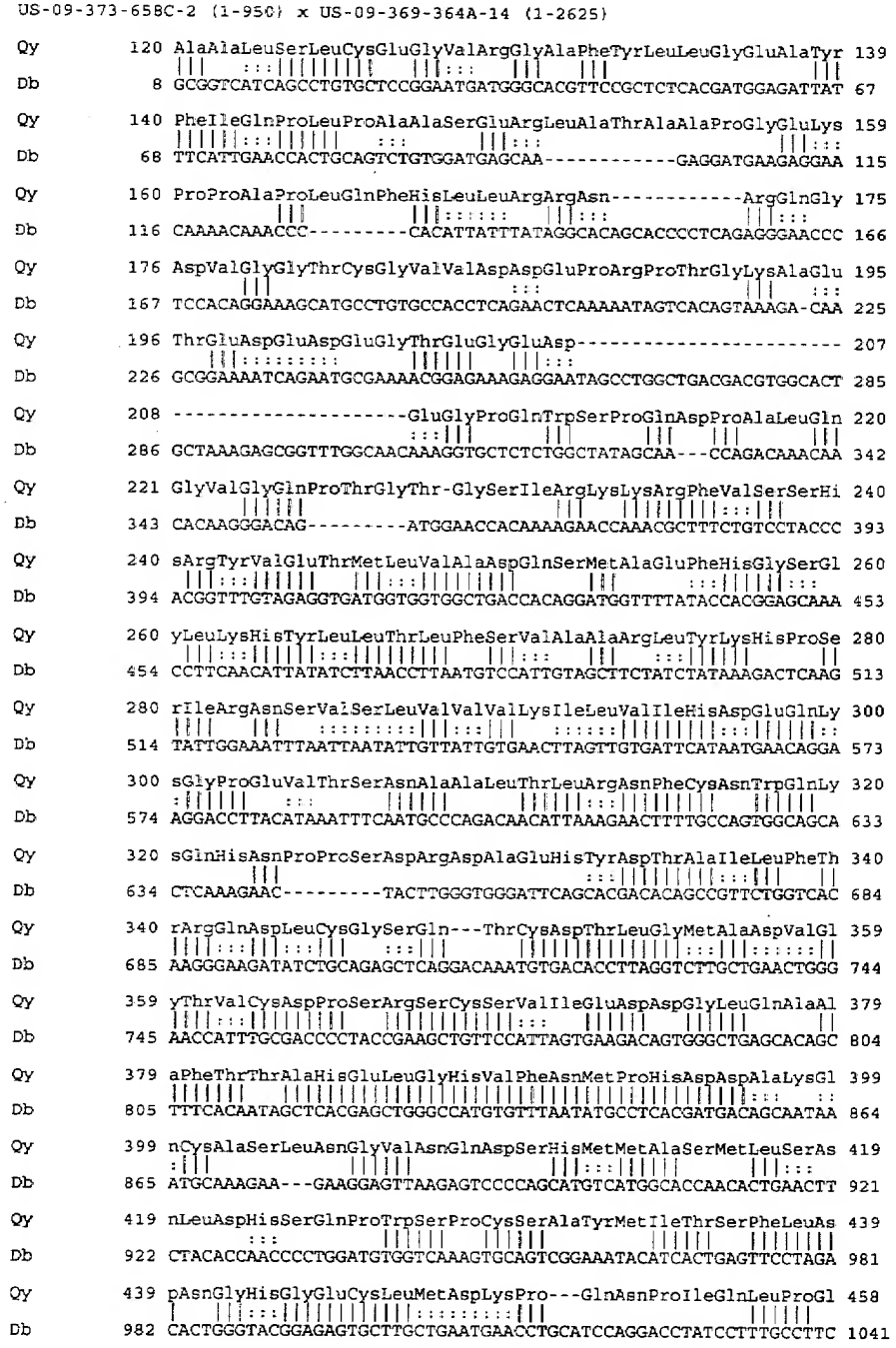


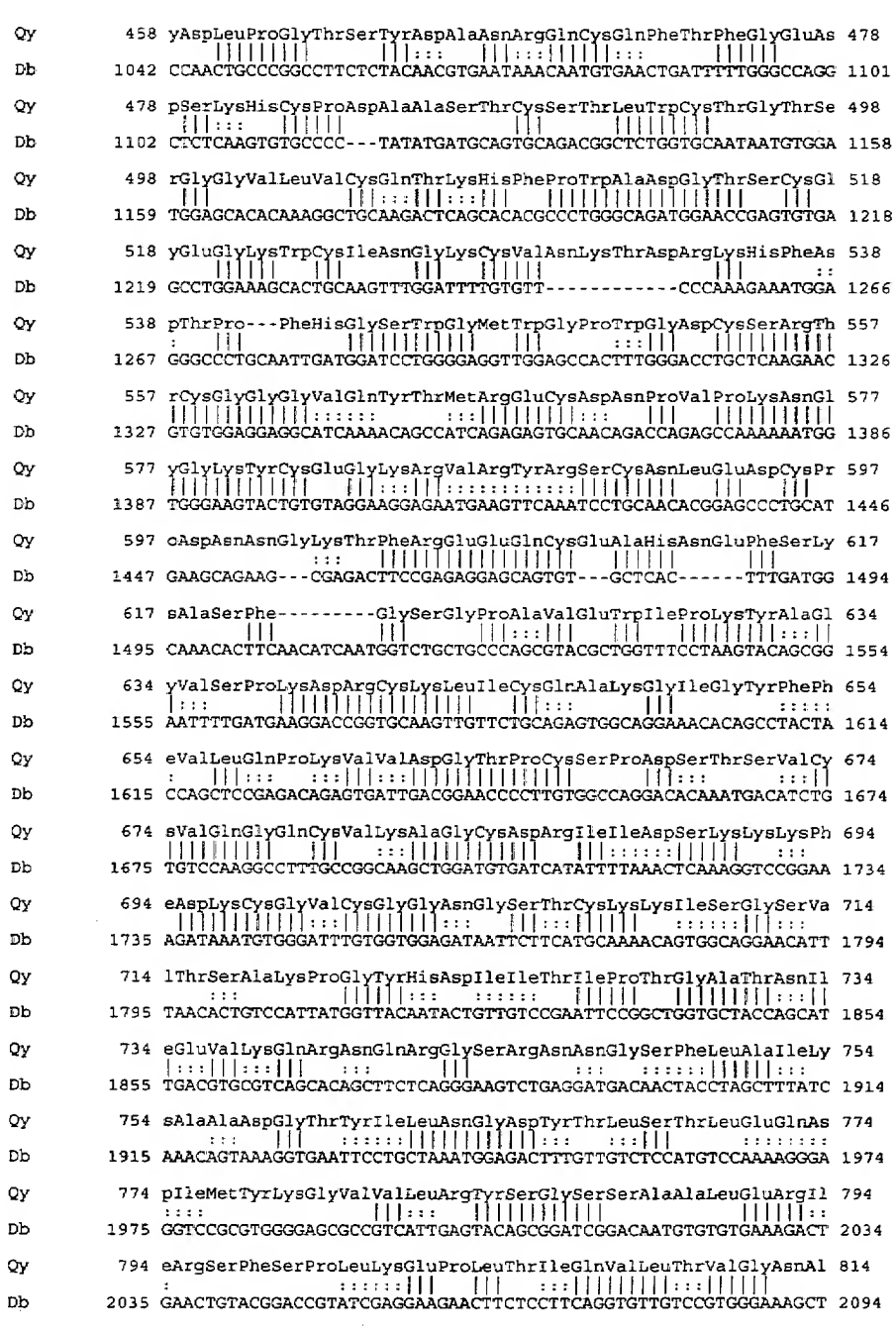
RESULT 15
US-09-369-364A-14
; Sequence 14, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Mus musculus ADAMTS-9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2623)
US-09-369-364A-14

Alignment Scores:

Pred. No.:	9.73e-139	Length:	2625
Score:	1611.00	Matches:	340
Percent Similarity:	55.99%	Conservative:	146
Best Local Similarity:	39.17%	Mismatches:	312
Query Match:	31.05%	Indels:	71
DB:	4	Gaps:	26

US-09-373-658C-2 (1-950) x US-09-369-364A-14 (1-2625)





```
Qy        814 aLeuArgProLysIleLysTyrThrTyrPhe------ValLysLysLysLysGluSerPh 832
Db       2095 GTATAACCCAGATGTGCGGTACTCATTCAATATTCCCATTGAGGACAAACCTCAGCAATT 2154

Qy        832 eAsnAlaIleProThrPheSerAlaTrpValIleGlu---GluTrpGlyGluCysSerLy 851
Db       2155 T--------------------TACTGGAACAGTCACGGGCCGTGGCAAGCATGCAGCAA 2193

Qy        851 sSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnPr 871
Db       2194 GCCCTGCCAAGGGGAGCGGAGACCAAAACTTGTTTGCACCAGGGAGTCTGATCAGCTAAC 2253

Qy        871 oAlaSerGlu------CysAlaLysGluValLysProAlaSer---ThrArgProCysAl 888
Db       2254 CGTTTCTGATCAAAGATGTGACCGGCTGCCCCAGCCAGGACCTGTCACTGAAGCGTGCGG 2313

Qy        888 aAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGl 908
Db       2314 CACAGACTGTGACTTGAGGTGGCACGTTGCCAGCAAGAGCGAATGCAGTGCCCAGTGTGG 2373

Qy        908 yLysGlyTyrLysLysArgSerLeuLysCysLeuSerHis---------AspGlyGlyVa 925
Db       2374 TTTGGGCTACCGTACTTTAGACATCCACTGTGCCAAATACAGCAGGATGGACGGGAAGAC 2433

Qy        925 l------LeuSerHisGluSerCysAspProLeuLysLysProLysHisPheIleAspPh 943
Db       2434 GGAGAAGGTGGATGACAGTTTCTGTAGCAGTCAACCCAGACCGAGTAAC---CAGGAGAA 2490

Qy        943 eCysThrMetAlaGluCysSer 950
Db       2491 ATGCTCA---GGAGAGTGCAGC 2509
```

Search completed: June 18, 2004, 19:00:01
Job time : 286.679 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 18:42:30 ; Search time 931.168 Seconds
(without alignments)
4673.735 Million cell updates/sec

Title: US-09-373-658C-2
Perfect score: 5189
Sequence: 1 MGNAERAPGSRSFGPVPTLL.....CDPLKKPKHFIDFCTMAECS 950

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09373658/runat_18062004_135345_10353/app_query.fasta_1.2254
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09373658_@CGN_1_1_1290_@runat_18062004_135345_10353
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5189	100.0	3261	10	US-09-373-658-1	Sequence 1, Appli
2	5189	100.0	3261	11	US-09-989-687-1	Sequence 1, Appli
3	5189	100.0	4014	15	US-10-115-286-1	Sequence 1, Appli
4	5189	100.0	4676	14	US-10-105-929-1	Sequence 1, Appli
5	5181	99.8	4309	15	US-10-210-120-57	Sequence 57, Appl
6	5181	99.8	4459	16	US-10-159-563-192	Sequence 192, App
7	5181	99.8	4459	16	US-10-159-563-308	Sequence 308, App
8	5181	99.8	4760	10	US-09-971-429B-17	Sequence 17, Appl
9	5144	99.1	4014	11	US-09-989-687-125	Sequence 125, App
10	5097.5	98.2	4848	13	US-10-425-114-26851	Sequence 26851, A
11	4299.5	82.9	4180	10	US-09-373-658-20	Sequence 20, Appl
12	4299.5	82.9	4180	11	US-09-989-687-20	Sequence 20, Appl
13	4292	82.7	4878	12	US-10-152-319A-1840	Sequence 1840, Ap
14	4292	82.7	4878	16	US-10-191-803-170	Sequence 170, App
15	3947	76.1	2184	9	US-09-445-023A-2	Sequence 2, Appli
16	3947	76.1	2184	15	US-10-097-597-2	Sequence 2, Appli
17	3947	76.1	2184	15	US-10-097-580-2	Sequence 2, Appli
18	3677	70.9	2184	9	US-09-445-023A-13	Sequence 13, Appl
19	3677	70.9	2184	15	US-10-097-597-13	Sequence 13, Appl
20	3677	70.9	2184	15	US-10-097-580-13	Sequence 13, Appl
21	3421	65.9	9248	10	US-09-373-658-21	Sequence 21, Appl
22	3421	65.9	9248	11	US-09-989-687-21	Sequence 21, Appl
23	3328	64.1	3147	9	US-09-803-589-1	Sequence 1, Appli
24	2667	51.4	3145	9	US-09-803-589-9	Sequence 9, Appli
25	2507.5	48.3	2804	16	US-10-093-463-27	Sequence 27, Appl
26	2494	48.1	3446	9	US-09-965-631-7	Sequence 7, Appli
27	2487	47.9	2853	9	US-09-965-631-3	Sequence 3, Appli
28	2483	47.9	2867	13	US-09-741-151-1	Sequence 1, Appli
29	2482.5	47.8	2937	13	US-10-275-107-24	Sequence 24, Appl
30	2465	47.5	2930	17	US-10-311-035-32	Sequence 32, Appl
31	2340	45.1	3008	10	US-09-373-658-3	Sequence 3, Appli
32	2340	45.1	3008	11	US-09-989-687-3	Sequence 3, Appli
33	2340	45.1	3711	17	US-10-283-975A-398	Sequence 398, App
34	2339	45.1	3715	13	US-10-425-114-26850	Sequence 26850, A
35	2284.5	44.0	3638	9	US-09-918-171A-8	Sequence 8, Appli
36	2203.5	42.5	2940	14	US-10-163-316-1	Sequence 1, Appli
37	2196.5	42.3	2469	14	US-10-163-316-3	Sequence 3, Appli
38	2173	41.9	4307	13	US-10-358-283-31	Sequence 31, Appl
39	2173	41.9	4307	16	US-10-191-997-121	Sequence 121, App
40	2168	41.8	4192	15	US-10-247-685-1	Sequence 1, Appli
41	2161	41.6	4407	10	US-09-946-374-316	Sequence 316, App
42	2161	41.6	4407	12	US-10-015-395A-316	Sequence 316, App
43	2161	41.6	4407	13	US-10-206-915-351	Sequence 351, App
44	2161	41.6	4407	13	US-10-199-670-351	Sequence 351, App
45	2161	41.6	4407	13	US-10-201-858-351	Sequence 351, App

ALIGNMENTS

RESULT 1
US-09-373-658-1
; Sequence 1, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```
;   NAME/KEY: CDS
;   LOCATION: (1)..(2853)
;   NAME/KEY: UNSURE
;   LOCATION: (3095)
;   OTHER INFORMATION: May be any nucleic acid
;   NAME/KEY: UNSURE
;   LOCATION: (3248)
;   OTHER INFORMATION: May be any nucleic acid
;   NAME/KEY: UNSURE
;   LOCATION: (3255)
;   OTHER INFORMATION: May be any nucleic acid
;   NAME/KEY: UNSURE
;   LOCATION: (3261)
;   OTHER INFORMATION: May be any nucleic acid
US-09-373-658-1

Alignment Scores:
Pred. No.:                0                Length:          3261
Score:                    5189.00          Matches:         950
Percent Similarity:       100.00%          Conservative:    0
Best Local Similarity:    100.00%          Mismatches:      0
Query Match:              100.00%          Indels:          0
DB:                       10               Gaps:            0

US-09-373-658C-2 (1-950) x US-09-373-658-1 (1-3261)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 60

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 120

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 180

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 240

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 300

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 360

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 420

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 480

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 540

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 600

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 660

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 720

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 780

Qy        261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 840

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 900

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 960

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1020

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1080

Qy        361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1140

Qy        381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1200

Qy        401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1260

Qy        421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1320

Qy        441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1380

Qy        461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1440

Qy        481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1500

Qy        501 ValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGly 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1560

Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 1620

Qy        541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1680

Qy        561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 1740

Qy        581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 1800
```

```
Qy        601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 1860

Qy        621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 1920

Qy        641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 1980

Qy        661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040

Qy        681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2100

Qy        701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2160

Qy        721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2220

Qy        741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2280

Qy        761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2340

Qy        781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2400

Qy        801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2460

Qy        821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520

Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2580

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2640

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2700

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 2760

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 2820

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950
              |||||||||||||||||||||||||||||
Db       2821 ATAGACTTTTGCACAATGGCAGAATGCAGT 2850

RESULT 2
```

```
US-09-989-687-1
; Sequence 1, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
;  APPLICANT: Hastings, Gregg A.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
;  FILE REFERENCE: 1488.107000D
;  CURRENT APPLICATION NUMBER: US/09/989,687
;  CURRENT FILING DATE:  2001-11-21
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3261
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2853)
;   NAME/KEY: misc_feature
;   LOCATION: (3195)
;   OTHER INFORMATION: n is any nucleic acid
;   NAME/KEY: misc_feature
;   LOCATION: (3248)
;   OTHER INFORMATION: n is any nucleic acid
;   NAME/KEY: misc_feature
;   LOCATION: (3255)
;   OTHER INFORMATION: n is any nucleic acid
;   NAME/KEY: misc_feature
;   LOCATION: (3261)
;   OTHER INFORMATION: n is any nucleic acid
US-09-989-687-1

Alignment Scores:
Pred. No.:                0              Length:          3261
Score:                    5189.00        Matches:         950
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       11             Gaps:            0

US-09-373-658C-2 (1-950) x US-09-989-687-1 (1-3261)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 60

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 120

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 180

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 240

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 300

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 360

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 420

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        421 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 480

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180

Db        481 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 540

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200

Db        541 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 600

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220

Db        601 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 660

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240

Db        661 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 720

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260

Db        721 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 780

Qy        261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280

Db        781 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 840

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300

Db        841 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 900

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320

Db        901 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 960

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340

Db        961 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1020

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360

Db       1021 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1080

Qy        361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380

Db       1081 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1140

Qy        381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400

Db       1141 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1200

Qy        401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420

Db       1201 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1260

Qy        421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440

Db       1261 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1320

Qy        441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460

Db       1321 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1380

Qy        461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480

Db       1381 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1440

Qy        481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500

Db       1441 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1500

Qy        501 ValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGly 520

Db       1501 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1560
```

```
Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540

Db       1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 1620

Qy        541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560

Db       1621 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1680

Qy        561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580

Db       1681 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 1740

Qy        581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600

Db       1741 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 1800

Qy        601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620

Db       1801 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 1860

Qy        621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640

Db       1861 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 1920

Qy        641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660

Db       1921 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 1980

Qy        661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680

Db       1981 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040

Qy        681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700

Db       2041 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2100

Qy        701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720

Db       2101 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2160

Qy        721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740

Db       2161 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2220

Qy        741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760

Db       2221 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2280

Qy        761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780

Db       2281 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2340

Qy        781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800

Db       2341 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2400

Qy        801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820

Db       2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2460

Qy        821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840

Db       2461 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520

Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860

Db       2521 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2580

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCys[illegible]aLysGluValLys 880

Db       2581 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2640
```

```
Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2700

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 2760

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 2820

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950
              |||||||||||||||||||||||||||||
Db       2821 ATAGACTTTTGCACAATGGCAGAATGCAGT 2850
```

RESULT 3
US-10-115-286-1
; Sequence 1, Application US/10115286
; Publication No. US20030166065A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hasting, Gregg
; TITLE OF INVENTION: No. US20030166065Aiel Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,286
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,496
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-115-286-1

Alignment Scores:

Pred. No.:	0	Length:	4014
Score:	5189.00	Matches:	950
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-373-658C-2 (1-950) x US-10-115-286-1 (1-4014)

```
Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 576

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 636

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 696

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 756

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 816

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 876

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 936

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 996

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 1056

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 1116

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 1176

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1236

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1296

Qy        261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1356

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1416

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1476

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1536

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1596
```

```
Qy       361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
Db      1597 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1656

Qy       381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
Db      1657 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1716

Qy       401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db      1717 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1776

Qy       421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
Db      1777 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1836

Qy       441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db      1837 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1896

Qy       461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db      1897 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1956

Qy       481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
Db      1957 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 2016

Qy       501 ValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db      2017 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 2076

Qy       521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
Db      2077 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 2136

Qy       541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
Db      2137 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 2196

Qy       561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
Db      2197 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 2256

Qy       581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
Db      2257 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 2316

Qy       601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
Db      2317 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2376

Qy       621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
Db      2377 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2436

Qy       641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db      2437 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2496

Qy       661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
Db      2497 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2556

Qy       681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700
Db      2557 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2616

Qy       701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db      2617 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2676

Qy       721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db      2677 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2736

Qy       741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
Db      2737 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2796

Qy       761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db      2797 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2856

Qy       781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
Db      2857 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2916

Qy       801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
Db      2917 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2976

Qy       821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db      2977 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 3036

Qy       841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
Db      3037 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 3096

Qy       861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
Db      3097 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 3156

Qy       881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db      3157 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 3216

Qy       901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
Db      3217 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 3276

Qy       921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
Db      3277 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 3336

Qy       941 IleAspPheCysThrMetAlaGluCysSer 950
Db      3337 ATAGACTTTTGCACAATGGCAGAATGCAGT 3366
```

RESULT 4
US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10/105,929
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (460)...(3360)
US-10-105-929-1

Alignment Scores:

Pred. No.:	0	Length:	4676
Score:	5189.00	Matches:	950
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-373-658C-2 (1-950) x US-10-105-929-1 (1-4676)

```
Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu  20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 570

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp  40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 630

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 690

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla  80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 750

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 810

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 870

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 930

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 990

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 1050

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 1110

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 1170

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1230

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1290

Qy        261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1350

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1410

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1470

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1530

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1590

Qy        361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1650

Qy        381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1710

Qy        401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1770

Qy        421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1830

Qy        441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1831 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1890

Qy        461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1950

Qy        481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1951 CACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 2010

Qy        501 ValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGly 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2011 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 2070

Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2071 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 2130

Qy        541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2131 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 2190

Qy        561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2191 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 2250

Qy        581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2251 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 2310

Qy        601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2311 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2370

Qy        621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2371 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2430

Qy        641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2431 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2490

Qy        661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
```

```
Db      2491 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2550

Qy       681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700

Db      2551 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2610

Qy       701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720

Db      2611 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2670

Qy       721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740

Db      2671 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2730

Qy       741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760

Db      2731 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2790

Qy       761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780

Db      2791 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2850

Qy       781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800

Db      2851 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2910

Qy       801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820

Db      2911 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2970

Qy       821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840

Db      2971 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 3030

Qy       841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860

Db      3031 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 3090

Qy       861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880

Db      3091 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 3150

Qy       881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900

Db      3151 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 3210

Qy       901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920

Db      3211 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 3270

Qy       921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940

Db      3271 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 3330

Qy       941 IleAspPheCysThrMetAlaGluCysSer 950

Db      3331 ATAGACTTTTGCACAATGGCAGAATGCAGT 3360
```

RESULT 5
US-10-210-120-57
; Sequence 57, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 4309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-57

Alignment Scores:

Pred. No.:	0	Length:	4309
Score:	5181.00	Matches:	949
Percent Similarity:	99.89%	Conservative:	0
Best Local Similarity:	99.89%	Mismatches:	1
Query Match:	99.85%	Indels:	0
DB:	15	Gaps:	0

US-09-373-658C-2 (1-950) x US-10-210-120-57 (1-4309)

```
Qy         1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20

Db       167 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCAGTACCCACGCTGCTG 226

Qy        21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40

Db       227 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 286

Qy        41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60

Db       287 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 346

Qy        61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80

Db       347 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 406

Qy        81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100

Db       407 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 466

Qy       101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120

Db       467 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 526

Qy       121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140

Db       527 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 586

Qy       141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160

Db       587 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 646

Qy       161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180

Db       647 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACG 706

Qy       181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200

Db       707 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 766

Qy       201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220

Db       767 GAAGGGACTGAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 826

Qy       221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240

Db       827 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 886

Qy       241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260

Db       887 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 946

Qy       261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
```

```
Db        947 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1006

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300

Db       1007 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1066

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320

Db       1067 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1126

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340

Db       1127 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1186

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360

Db       1187 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1246

Qy        361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380

Db       1247 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1306

Qy        381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400

Db       1307 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1366

Qy        401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420

Db       1367 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1426

Qy        421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440

Db       1427 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1486

Qy        441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460

Db       1487 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1546

Qy        461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480

Db       1547 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1606

Qy        481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500

Db       1607 CACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1666

Qy        501 ValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGly 520

Db       1667 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1726

Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540

Db       1727 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 1786

Qy        541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560

Db       1787 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1846

Qy        561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580

Db       1847 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 1906

Qy        581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600

Db       1907 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 1966

Qy        601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620

Db       1967 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2026

Qy        621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640

Db       2027 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2086

Qy        641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660

Db       2087 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2146

Qy        661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680

Db       2147 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2206

Qy        681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700

Db       2207 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2266

Qy        701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720

Db       2267 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2326

Qy        721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740

Db       2327 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2386

Qy        741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760

Db       2387 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2446

Qy        761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780

Db       2447 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2506

Qy        781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800

Db       2507 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2566

Qy        801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820

Db       2567 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2626

Qy        821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840

Db       2627 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2686

Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860

Db       2687 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2746

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880

Db       2747 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2806

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900

Db       2807 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2866

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920

Db       2867 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 2926

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940

Db       2927 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 2986

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950

Db       2987 ATAGACTTTTGCACAATGGCAGAATGCAGT 3016
```

RESULT 6
US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus

```
;  APPLICANT:  Peterson, Carsten
;  APPLICANT:  Meltzer, Paul
;  TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
;  TITLE OF INVENTION:  DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
;  FILE REFERENCE: 11613.56USI1
;  CURRENT APPLICATION NUMBER: US/10/159,563
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 10/133,937
;  PRIOR FILING DATE: 2002-04-25
;  NUMBER OF SEQ ID NOS: 444
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
;   LENGTH: 4459
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-159-563-192

Alignment Scores:
Pred. No.:                0          Length:          4459
Score:                    5181.00    Matches:         949
Percent Similarity:       99.89%     Conservative:    0
Best Local Similarity:    99.89%     Mismatches:      1
Query Match:              99.85%     Indels:          0
DB:                       16         Gaps:            0

US-09-373-658C-2 (1-950) x US-10-159-563-192 (1-4459)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 353

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 413

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 473

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 533

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 593

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 653

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 713

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 773

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACG 833

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 893

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 GAAGGGACTGAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 953

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        954 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1013

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1073

Qy        261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1133

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1193

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1253

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1254 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1313

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1314 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1373

Qy        361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1433

Qy        381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1493

Qy        401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1553

Qy        421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1613

Qy        441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1673

Qy        461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1733

Qy        481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 CACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1793

Qy        501 ValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGly 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1853

Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 1913

Qy        541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1973

Qy        561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1974 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 2033

Qy        581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2034 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 2093
```

```
Qy        601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
Db       2094 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2153

Qy        621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
Db       2154 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2213

Qy        641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db       2214 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2273

Qy        661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
Db       2274 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2333

Qy        681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700
Db       2334 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2393

Qy        701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db       2394 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2453

Qy        721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db       2454 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2513

Qy        741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
Db       2514 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2573

Qy        761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db       2574 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2633

Qy        781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
Db       2634 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2693

Qy        801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
Db       2694 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2753

Qy        821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db       2754 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2813

Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
Db       2814 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2873

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
Db       2874 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2933

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db       2934 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2993

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
Db       2994 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 3053

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
Db       3054 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 3113

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950
Db       3114 ATAGACTTTTGCACAATGGCAGAATGCAGT 3143
```

```
RESULT 7
US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
;  APPLICANT: Khan, Javed
;  APPLICANT:  Ringner, Markus
;  APPLICANT:  Peterson, Carsten
;  APPLICANT:  Meltzer, Paul
;  TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
;  TITLE OF INVENTION:  DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
;  FILE REFERENCE: 11613.56USI1
;  CURRENT APPLICATION NUMBER: US/10/159,563
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 10/133,937
;  PRIOR FILING DATE: 2002-04-25
;  NUMBER OF SEQ ID NOS: 444
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
;   LENGTH: 4459
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-159-563-308

Alignment Scores:
Pred. No.:                0              Length:          4459
Score:                    5181.00        Matches:         949
Percent Similarity:       99.89%         Conservative:    0
Best Local Similarity:    99.89%         Mismatches:      1
Query Match:              99.85%         Indels:          0
DB:                       16             Gaps:            0

US-09-373-658C-2 (1-950) x US-10-159-563-308 (1-4459)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db        294 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 353

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
Db        354 CTGCTCGCCGCGGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 413

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
Db        414 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 473

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
Db        474 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 533

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db        534 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 593

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db        594 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 653

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
Db        654 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 713

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
Db        714 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 773

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
Db        774 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACG 833

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db        834 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 893
```

```
Qy      201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db      894 GAAGGGACTGAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 953

Qy      221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
Db      954 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1013

Qy      241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db      1014 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1073

Qy      261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
Db      1074 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1133

Qy      281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
Db      1134 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1193

Qy      301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db      1194 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTGCAACTGGCAGAAG 1253

Qy      321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
Db      1254 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1313

Qy      341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db      1314 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1373

Qy      361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
Db      1374 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1433

Qy      381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
Db      1434 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1493

Qy      401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db      1494 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1553

Qy      421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
Db      1554 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1613

Qy      441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db      1614 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1673

Qy      461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db      1674 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1733

Qy      481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
Db      1734 CACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1793

Qy      501 ValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db      1794 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1853

Qy      521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
Db      1854 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 1913

Qy      541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
Db      1914 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1973

Qy      561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
Db      1974 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 2033

Qy      581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
Db      2034 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 2093

Qy      601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
Db      2094 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2153

Qy      621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
Db      2154 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2213

Qy      641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db      2214 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2273

Qy      661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
Db      2274 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2333

Qy      681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700
Db      2334 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2393

Qy      701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db      2394 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2453

Qy      721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db      2454 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2513

Qy      741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
Db      2514 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2573

Qy      761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db      2574 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2633

Qy      781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
Db      2634 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2693

Qy      801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
Db      2694 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2753

Qy      821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db      2754 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2813

Qy      841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
Db      2814 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2873

Qy      861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
Db      2874 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2933

Qy      881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db      2934 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2993

Qy      901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
Db      2994 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 3053

Qy      921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3054 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 3113

Qy         941 IleAspPheCysThrMetAlaGluCysSer 950
               ||||||||||||||||||||||||||||||
Db        3114 ATAGACTTTTGCACAATGGCAGAATGCAGT 3143

RESULT 8
US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
;  APPLICANT: Lasek, Amy K. W.
;  APPLICANT:  Shyjan, Andrew W.
;  APPLICANT:  Turner, Christopher M.
;  TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
;  FILE REFERENCE: PA-0040 US
;  CURRENT APPLICATION NUMBER: US/09/971,429B
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/239,024
;  PRIOR FILING DATE: 2000-04-10
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PERL Program
; SEQ ID NO 17
;   LENGTH: 4760
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 118
;   OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17

Alignment Scores:
Pred. No.:              0            Length:         4760
Score:                  5181.00      Matches:        949
Percent Similarity:     99.89%       Conservative:   0
Best Local Similarity:  99.89%       Mismatches:     1
Query Match:            99.85%       Indels:         0
DB:                     10           Gaps:           0

US-09-373-658C-2 (1-950) x US-09-971-429B-17 (1-4760)

Qy           1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         612 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCAGTACCCACGCTGCTG 671

Qy          21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         672 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 731

Qy          41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         732 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 791

Qy          61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         792 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 851

Qy          81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         852 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 911

Qy         101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         912 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 971

Qy         121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         972 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 1031

Qy         141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1032 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 1091

Qy         161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1092 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 1151

Qy         181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1152 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 1211

Qy         201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1212 GAAGGGACTGAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 1271

Qy         221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1272 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1331

Qy         241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1332 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1391

Qy         261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1392 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1451

Qy         281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1452 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1511

Qy         301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1512 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1571

Qy         321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1572 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1631

Qy         341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1632 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1691

Qy         361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1692 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1751

Qy         381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1752 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1811

Qy         401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1812 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1871

Qy         421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1872 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1931

Qy         441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1932 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1991

Qy         461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1992 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 2051

Qy         481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2052 CACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 2111
```

```
Qy        501 ValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db       2112 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 2171

Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
Db       2172 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 2231

Qy        541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
Db       2232 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 2291

Qy        561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
Db       2292 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 2351

Qy        581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
Db       2352 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 2411

Qy        601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
Db       2412 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2471

Qy        621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
Db       2472 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2531

Qy        641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db       2532 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2591

Qy        661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
Db       2592 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2651

Qy        681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700
Db       2652 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2711

Qy        701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db       2712 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2771

Qy        721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db       2772 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2831

Qy        741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
Db       2832 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2891

Qy        761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db       2892 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2951

Qy        781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
Db       2952 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 3011

Qy        801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
Db       3012 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 3071

Qy        821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db       3072 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 3131

Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
Db       3132 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 3191

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
Db       3192 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 3251

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db       3252 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 3311

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
Db       3312 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 3371

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
Db       3372 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 3431

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950
Db       3432 ATAGACTTTTGCACAATGGCAGAATGCAGT 3461
```

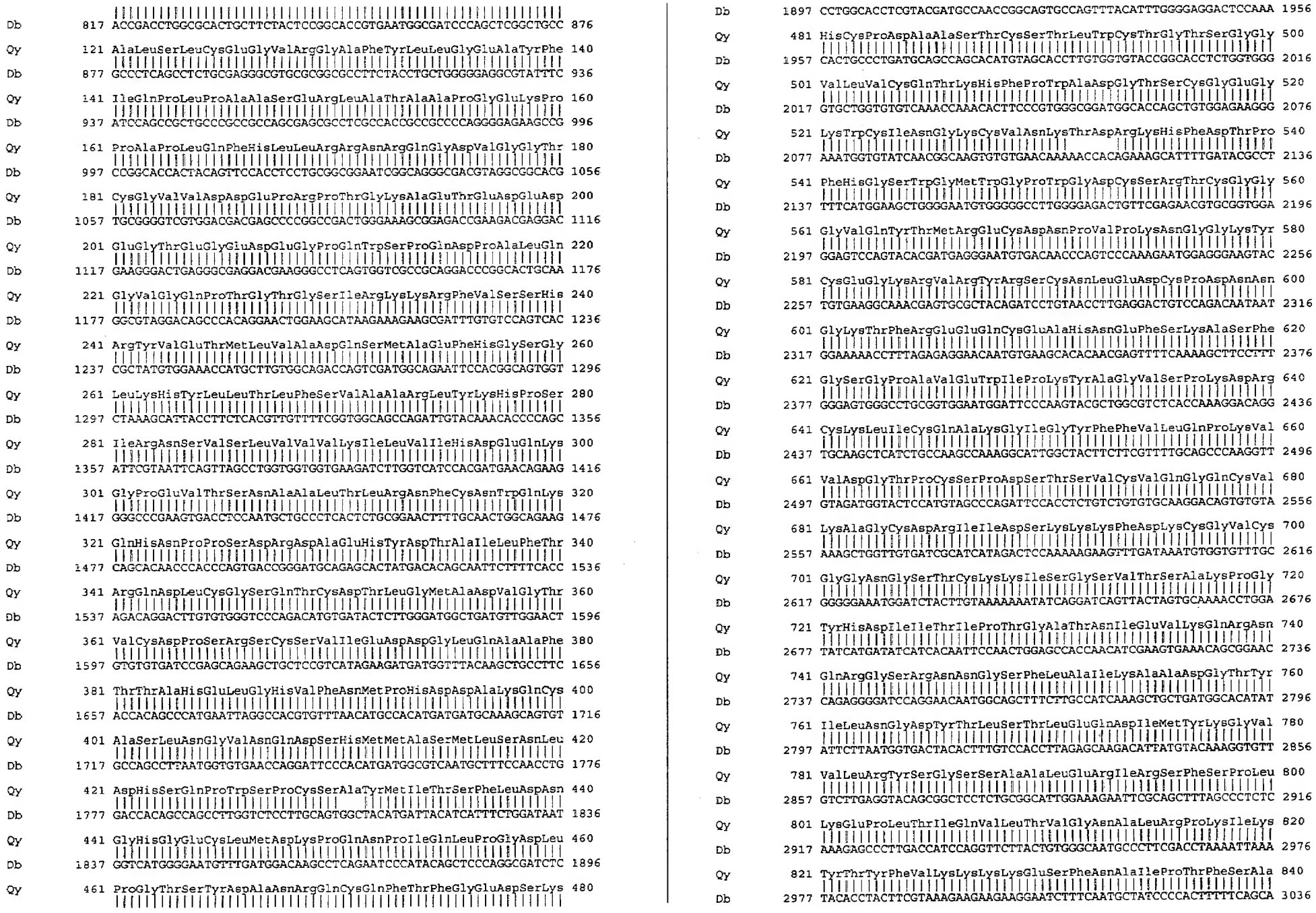
RESULT 9
US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (466)..(3366)
; OTHER INFORMATION:
US-09-989-687-125

Alignment Scores:

Pred. No.:	0	Length:	4014
Score:	5144.00	Matches:	940
Percent Similarity:	99.37%	Conservative:	4
Best Local Similarity:	98.95%	Mismatches:	6
Query Match:	99.13%	Indels:	0
DB:	11	Gaps:	0

US-09-373-658C-2 (1-950) x US-09-989-687-125 (1-4014)

```
Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db        517 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 576

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
Db        577 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 636

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
Db        637 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGTCCCGGGACACGGGACCACGCGCCTCCGC 696

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
Db        697 CTGCACGCCTTTGACCAGCAGCTGGATCTGGACGTGCCGCCCGACAGCAGCTTTTTGGCG 756

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db        757 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGACACCCCGCTTCCGGAA 816

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
```


Db 817 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 876
Qy 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
Db 877 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 936
Qy 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
Db 937 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 996
Qy 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
Db 997 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 1056
Qy 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db 1057 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 1116
Qy 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db 1117 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 1176
Qy 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
Db 1177 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1236
Qy 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db 1237 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1296
Qy 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
Db 1297 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1356
Qy 281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
Db 1357 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1416
Qy 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db 1417 GGGCCCGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1476
Qy 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
Db 1477 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1536
Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db 1537 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1596
Qy 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
Db 1597 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1656
Qy 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
Db 1657 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1716
Qy 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db 1717 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1776
Qy 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
Db 1777 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGGCTACATGATTACATCATTTCTGGATAAT 1836
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db 1837 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1896
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db 1897 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1956
Qy 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
Db 1957 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 2016
Qy 501 ValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db 2017 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 2076
Qy 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
Db 2077 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAAACCACAGAAAGCATTTTGATACGCCT 2136
Qy 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
Db 2137 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 2196
Qy 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
Db 2197 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 2256
Qy 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
Db 2257 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 2316
Qy 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
Db 2317 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 2376
Qy 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
Db 2377 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 2436
Qy 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db 2437 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 2496
Qy 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
Db 2497 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2556
Qy 681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700
Db 2557 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2616
Qy 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db 2617 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2676
Qy 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db 2677 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2736
Qy 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
Db 2737 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2796
Qy 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db 2797 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2856
Qy 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
Db 2857 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2916
Qy 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
Db 2917 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2976
Qy 821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db 2977 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 3036

```
Qy        841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3037 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 3096

Qy        861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3097 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 3156

Qy        881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3157 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 3216

Qy        901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3217 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAACAAGCTTGAAGTGTCTGTCC 3276

Qy        921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       3277 CATGATGGAGGGGTGTTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 3336

Qy        941 IleAspPheCysThrMetAlaGluCysSer 950
              |||||||||||||||||||||||||||||
Db       3337 ATAGACTTTTGCACAATGGCAGAATGCAGT 3366

RESULT 10
US-10-425-114-26851
; Sequence 26851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26851
;   LENGTH: 4848
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4654-036-D4_FLI
US-10-425-114-26851

Alignment Scores:
Pred. No.:              0              Length:          4848
Score:                  5097.50        Matches:         949
Percent Similarity:     92.86%         Conservative:    0
Best Local Similarity:  92.86%         Mismatches:      1
Query Match:            98.24%         Indels:          73
DB:                     13             Gaps:            1

US-09-373-658C-2 (1-950) x US-10-425-114-26851 (1-4848)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 552

Qy         21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 612

Qy         41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 672

Qy         61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 732

Qy         81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 792

Qy        101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 852

Qy        121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 912

Qy        141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 972

Qy        161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 1032

Qy        181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 TGCGGGGTGGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 1092

Qy        201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 1152

Qy        221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 1212

Qy        241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 1272

Qy        261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 1332

Qy        281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 1392

Qy        301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 1452

Qy        321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1512

Qy        341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1572

Qy        361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1573 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1632

Qy        381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1633 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1692

Qy        401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1693 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1752

Qy        421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1753 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1812
Qy        441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db       1813 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCATA-CAGCTCCCAGGCGATCTC 1871
Qy        461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db       1872 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1931
Qy        481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
Db       1932 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1991
Qy        501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db       1992 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 2051
Qy        521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAsp------ 538
Db       2052 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATGTGAGT 2111
Qy        538 ------------------------------------------------------------ 538
Db       2112 TTTTCTACTGAAACACATTCAGAATTGAAAAGAACAAAGTGATGGTAAAAGATATGATAC 2171
Qy        538 ------------------------------------------------------------ 538
Db       2172 CAAGTTAAACATCCCCATCCGTGTCCTCTAGCAGGAATGCGAGATAGCTTATTTTTAGAA 2231
Qy        538 ------------------------------------------------------------ 538
Db       2232 CTGATTCTTTGTCCCATGTGGCTTTCTTTGATACCCTAAAAGTTCTCTTTAGATAATTCT 2291
Qy        539 ----------------------------ThrProPheHisGlySerTrpGlyMetTrpGl 549
Db       2292 AATGCTGATGATTTATGTCTCCATTTAGACGCCTTTTCATGGAAGCTGGGGAATGTGGGG 2351
Qy        549 yProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCy 569
Db       2352 GCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATG 2411
Qy        569 sAspAsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrAr 589
Db       2412 TGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAG 2471
Qy        589 gSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCy 609
Db       2472 ATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATG 2531
Qy        609 sGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIl 629
Db       2532 TGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGAT 2591
Qy        629 eProLysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGl 649
Db       2592 TCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGG 2651
Qy        649 yIleGlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAs 669
Db       2652 CATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCAGA 2711
Qy        669 pSerThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAs 689
Db       2712 TTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGA 2771
Qy        689 pSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLy 709
Db       2772 CTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAATGGATCTACTTGTAAAAA 2831
Qy        709 sIleSerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProTh 729
Db       2832 AATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGATATCATCACAATTCCAAC 2891
```

```
Qy        729 rGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySe 749
Db       2892 TGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGCAG 2951
Qy        749 rPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSe 769
Db       2952 CTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAATGGTGACTACACTTTGTC 3011
Qy        769 rThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAl 789
Db       3012 CACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGGTACAGCGGCTCCTCTGC 3071
Qy        789 aAlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLe 809
Db       3072 GGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCT 3131
Qy        809 uThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLy 829
Db       3132 TACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTACTTCGTAAAGAAGAAGAA 3191
Qy        829 sGluSerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCy 849
Db       3192 GGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATTGAAGAGTGGGGCGAATG 3251
Qy        849 sSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGl 869
Db       3252 TTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGG 3311
Qy        869 yGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs 889
Db       3312 ACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGA 3371
Qy        889 pHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLy 909
Db       3372 CCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAA 3431
Qy        909 sGlyTyrLysLysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGl 929
Db       3432 GGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGA 3491
Qy        929 uSerCysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCy 949
Db       3492 GAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTTTGCACAATGGCAGAATG 3551
Qy        949 sSer 950
Db       3552 CAGT 3555
```

```
RESULT 11
US-09-373-658-20
; Sequence 20, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
;  APPLICANT: Iruela-Arispe, Luisa
;  APPLICANT:  Hastings, Gregg A.
;  APPLICANT:  Ruben, Steven M.
;  APPLICANT:  Jonak, Zdenka L.
;  APPLICANT:  Trulli, Stephen H.
;  APPLICANT:  Fronwald, James A.
;  APPLICANT:  Terrett, Jonathan A.
;  TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
;  FILE REFERENCE: 1488.1070006
;  CURRENT APPLICATION NUMBER: US/09/373,658
;  CURRENT FILING DATE:  1999-08-13
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 4180
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:Unknown
```

US-09-373-658-20

Alignment Scores:

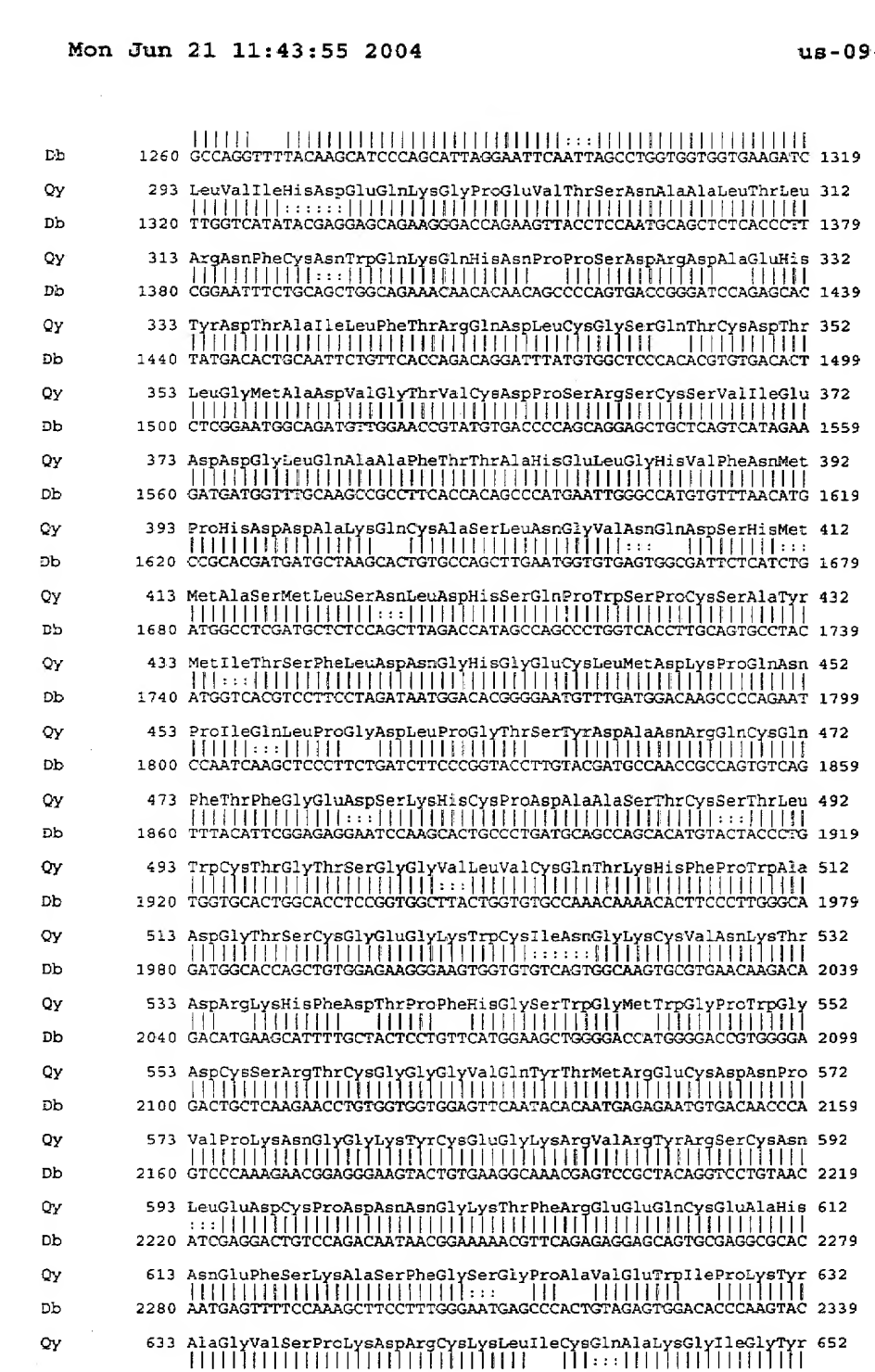
Pred. No.:	0	Length:	4180
Score:	4299.50	Matches:	789
Percent Similarity:	88.31%	Conservative:	57
Best Local Similarity:	82.36%	Mismatches:	97
Query Match:	82.86%	Indels:	15
DB:	10	Gaps:	5

US-09-373-658C-2 (1-950) x US-09-373-658-20 (1-4180)

```
Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db        441 ATGGGGGACGTCCAGCGGGCAGCGAGATCTCGGGGCTCTCTGTCCGCACACATGCTGTTG 500

Qy         21 LeuLeuAlaAlaAla---------LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37
Db        501 CTGCTCCTCGCTTCCATAACAATGCTGCTATGTGCGCGGGGCGCACACGGGCGCCCCACG 560

Qy         38 GluGluAspGluGluLeuValValProGluLeuGluArgAlaProGlyHisGly------ 55
Db        561 GAGGAAGATGAGGAGCTGGTCCTGCCCTCGCTGGAGCGCGCCCCGGGCCACGATTCCACC 620

Qy         56 ThrThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAsp 75
Db        621 ACCACACGCCTTCGTCTGGACGCCTTTGGCCAGCAGCTACATCTGAAGTTGCAGCCGGAC 680

Qy         76 SerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGlu 95
Db        681 AGCGGTTTCTTGGCGCCTGGCTTCACCCTGCAGACTGTGGGGCGCAGTCCCGGGTCCGAG 740

Qy         96 ThrProLeu------ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsn 113
Db        741 GCACAACATCTGGACCCCACCGGGGACCTGGCTCACTGCTTCTACTCTGGCACGGTGAAC 800

Qy        114 GlyAspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyr 133
Db        801 GGTGATCCCGGCTCTGCCGCAGCCCTCAGCCTCTGTGAAGGTGTGCGTGGTGCCTTCTAC 860

Qy        134 LeuLeuGlyGluAlaTyrPheIleGlnProLeuPro---AlaAlaSerGluArgLeuAla 152
Db        861 CTACAAGGAGAGGAGTTCTTCATTCAGCCAGCGCCTGGAGTGGCCACCGAGCGCCTGGCC 920

Qy        153 ThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172
Db        921 CCTGCCGTGCCCGAGGAGGAGTCATCCGCACGGCCGCAGTTCCACATCCTGAGGCGAAGG 980

Qy        173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192
Db        981 CGGCGGGGCAGTGGCGGCGCCAAGTGCGGCGTCATGGACGACGAGACCCTGCCAACC--- 1037

Qy        193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212
Db       1038 ------------------AGCGACTCGCGACCCGAGAGCCAGAACACCCGGAACCAGTGG 1079

Qy        213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232
Db       1080 CCTGTGCGGGACCCCACGCCTCAGGACGCGGGAAAGCCATCAGGACCAGGAAGCATAAGG 1139

Qy        233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252
Db       1140 AAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTAGCTGACCAGTCC 1199

Qy        253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272
Db       1200 ATGGCCGACTTCCACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTCTCGGTGGCA 1259

Qy        273 AlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIle 292
Db       1260 GCCAGGTTTTACAAGCATCCCAGCATTAGGAATTCAATTAGCCTGGTGGTGGTGAAGATC 1319

Qy        293 LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeu 312
```

```
Db       1320 TTGGTCATATACGAGGAGCAGAAGGGACCAGAAGTTACCTCCAATGCAGCTCTCACCCTT 1379

Qy        313 ArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis 332
Db       1380 CGGAATTTCTGCAGCTGGCAGAAACAACACAACAGCCCCAGTGACCGGGATCCAGAGCAC 1439

Qy        333 TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThr 352
Db       1440 TATGACACTGCAATTCTGTTCACCAGACAGGATTTATGTGGCTCCCACACGTGTGACACT 1499

Qy        353 LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu 372
Db       1500 CTCGGAATGGCAGATGTTGGAACCGTATGTGACCCCAGCAGGAGCTGCTCAGTCATAGAA 1559

Qy        373 AspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMet 392
Db       1560 GATGATGGTTTGCAAGCCGCCTTCACCACAGCCCATGAATTGGGCCATGTGTTTAACATG 1619

Qy        393 ProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMet 412
Db       1620 CCGCACGATGATGCTAAGCACTGTGCCAGCTTGAATGGTGTGAGTGGCGATTCTCATCTG 1679

Qy        413 MetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyr 432
Db       1680 ATGGCCTCGATGCTCTCCAGCTTAGACCATAGCCAGCCCTGGTCACCTTGCAGTGCCTAC 1739

Qy        433 MetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsn 452
Db       1740 ATGGTCACGTCCTTCCTAGATAATGGACACGGGGAATGTTTGATGGACAAGCCCCAGAAT 1799

Qy        453 ProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGln 472
Db       1800 CCAATCAAGCTCCCTTCTGATCTTCCCGGTACCTTGTACGATGCCAACCGCCAGTGTCAG 1859

Qy        473 PheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeu 492
Db       1860 TTTACATTCGGAGAGGAATCCAAGCACTGCCCTGATGCAGCCAGCACATGTACTACCCTG 1919

Qy        493 TrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProProTrpAla 512
Db       1920 TGGTGCACTGGCACCTCCGGTGGCTTACTGGTGTGCCAAACAAAACACTTCCCTTGGGCA 1979

Qy        513 AspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThr 532
Db       1980 GATGGCACCAGCTGTGGAGAAGGGAAGTGGTGTGTCAGTGGCAAGTGCGTGAACAAGACA 2039

Qy        533 AspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGly 552
Db       2040 GACATGAAGCATTTTGCTACTCCTGTTCATGGAAGCTGGGGACCATGGGGACCGTGGGGA 2099

Qy        553 AspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnPro 572
Db       2100 GACTGCTCAAGAACCTGTGGTGGTGGAGTTCAATACACAATGAGAGAATGTGACAACCCA 2159

Qy        573 ValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsn 592
Db       2160 GTCCCAAAGAACGGAGGGAAGTACTGTGAAGGCAAACGAGTCCGCTACAGGTCCTGTAAC 2219

Qy        593 LeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHis 612
Db       2220 ATCGAGGACTGTCCAGACAATAACGGAAAAACGTTCAGAGAGGAGCAGTGCGAGGCGCAC 2279

Qy        613 AsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyr 632
Db       2280 AATGAGTTTTCCAAAGCTTCCTTTGGGAATGAGCCCACTGTAGAGTGGACACCCAAGTAC 2339

Qy        633 AlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyr 652
Db       2340 GCCGGCGTCTCGCCAAAGGACAGGTGCAAGCTCACCTGTGAAGCCAAAGGCATTGGCTAC 2399

Qy        653 PhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSer 672
```

```
Db       2400 TTTTTCGTCTTACAGCCCAAGGTTGTAGATGGCACTCCCTGTAGTCCAGACTCTACCTCT 2459

Qy        673 ValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLys 692

Db       2460 GTCTGTGTGCAAGGGCAGTGTGTGAAAGCTGGCTGTGATCGCATCATAGACTCCAAAAAG 2519

Qy        693 LysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGly 712

Db       2520 AAGTTTGATAAGTGTGGCGTTTGTGGAGGAAACGGTTCCACATGCAAGAAGATGTCAGGA 2579

Qy        713 SerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThr 732

Db       2580 ATAGTCACTAGTACAAGACCTGGGTATCATGACATTGTCACAATTCCTGCTGGAGCCACC 2639

Qy        733 AsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAla 752

Db       2640 AACATTGAAGTGAAACATCGGAATCAAAGGGGGTCCAGAAACAATGGCAGCTTTCTGGCT 2699

Qy        753 IleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGlu 772

Db       2700 ATTAGAGCCGCTGATGGTACCTATATTCTGAATGGAAACTTCACTCTGTCCACACTAGAG 2759

Qy        773 GlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGlu 792

Db       2760 CAAGACCTCACCTACAAAGGTACTGTCTTAAGGTACAGTGGTTCCTCGGCTGCGCTGGAA 2819

Qy        793 ArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGly 812

Db       2820 AGAATCCGCAGCTTTAGTCCACTCAAAGAACCCTTAACCATCCAGGTTCTTATGGTAGGC 2879

Qy        813 AsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPhe 832

Db       2880 CATGCTCTCCGACCCAAAATTAAATTCACCTACTTTATGAAGAAGAAGACAGAGTCATTC 2939

Qy        833 AsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSer 852

Db       2940 AACGCCATTCCCACATTTTCTGAGTGGGTGATTGAAGAGTGGGGGGAGTGCTCCAAGACA 2999

Qy        853 CysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAla 872

Db       3000 TGCGGCTCAGGTTGGCAGAGAAGAGTAGTGCAGTGCAGAGACATTAACGGACACCCTGCT 3059

Qy        873 SerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 892

Db       3060 TCCGAATGTGCAAAGGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGACCTTCCTTGC 3119

Qy        893 ProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLys 912

Db       3120 CCACACTGGCAGGTGGGGGATTGGTCACCATGTTCCAAAACTTGCGGGAAGGGTTACAAG 3179

Qy        913 LysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAsp 932

Db       3180 AAGAGAACCTTGAAATGTGTGTCCCACGATGGGGGCGTGTTATCAAATGAGAGCTGTGAT 3239

Qy        933 ProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950

Db       3240 CCTTTGAAGAAGCCAAAGCATTACATTGACTTTTGCACACTGACACAGTGCAGT 3293

RESULT 12
US-09-989-687-20
; Sequence 20, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
;  APPLICANT: Hastings, Gregg A.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
;  FILE REFERENCE: 1488.107000D
;  CURRENT APPLICATION NUMBER: US/09/989,687
;  CURRENT FILING DATE:  2001-11-21
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 4180
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:Unknown
US-09-989-687-20

Alignment Scores:
Pred. No.:                0          Length:          4180
Score:                    4299.50    Matches:         789
Percent Similarity:       88.31%     Conservative:    57
Best Local Similarity:    82.36%     Mismatches:      97
Query Match:              82.86%     Indels:          15
DB:                       11         Gaps:            5

US-09-373-658C-2 (1-950) x US-09-989-687-20 (1-4180)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20

Db        441 ATGGGGGACGTCCAGCGGGCAGCGAGATCTCGGGGCTCTCTGTCCGCACACATGCTGTTG 500

Qy         21 LeuLeuAlaAlaAla---------LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37

Db        501 CTGCTCCTCGCTTCCATAACAATGCTGCTATGTGCGCGGGGCGCACACGGGCGCCCCACG 560

Qy         38 GluGluAspGluGluLeuValValProGluLeuGluArgAlaProGlyHisGly------ 55

Db        561 GAGGAAGATGAGGAGCTGGTCCTGCCCTCGCTGGAGCGCGCCCCGGGCCACGATTCCACC 620

Qy         56 ThrThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAsp 75

Db        621 ACCACACGCCTTCGTCTGGACGCCTTTGGCCAGCAGCTACATCTGAAGTTGCAGCCGGAC 680

Qy         76 SerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGlu 95

Db        681 AGCGGTTTCTTGGCGCCTGGCTTCACCCTGCAGACTGTGGGGCGCAGTCCCGGGTCCGAG 740

Qy         96 ThrProLeu------ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsn 113

Db        741 GCACAACATCTGGACCCCACCGGGGACCTGGCTCACTGCTTCTACTCTGGCACGGTGAAC 800

Qy        114 GlyAspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyr 133

Db        801 GGTGATCCCGGCTCTGCCGCAGCCCTCAGCCTCTGTGAAGGTGTGCGTGGTGCCTTCTAC 860

Qy        134 LeuLeuGlyGluAlaTyrPheIleGlnProLeuPro---AlaAlaSerGluArgLeuAla 152

Db        861 CTACAAGGAGAGGAGTTCTTCATTCAGCCAGCGCCTGGAGTGGCCACCGAGCGCCTGGCC 920

Qy        153 ThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172

Db        921 CCTGCCGTGCCCGAGGAGGAGTCATCCGCACGGCCGCAGTTCCACATCCTGAGGCGAAGG 980

Qy        173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192

Db        981 CGGCGGGGCAGTGGCGGCGCCAAGTGCGGCGTCATGGACGACGAGACCCTGCCAACC--- 1037

Qy        193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212

Db       1038 -----------------AGCGACTCGCGACCCGAGAGCCAGAACACCCGGAACCAGTGG 1079

Qy        213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232

Db       1080 CCTGTGCGGGACCCCACGCCTCAGGACGCGGGAAAGCCATCAGGACCAGGAAGCATAAGG 1139

Qy        233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252

Db       1140 AAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTAGCTGACCAGTCC 1199

Qy        253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272

Db       1200 ATGGCCGACTTCCACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTCTCGGTGGCA 1259

Qy        273 AlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIle 292
```



RESULT 13
US-10-152-319A-1840
; Sequence 1840, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael

```
;  TITLE OF INVENTION: Molecular Toxicology Modeling
;  FILE REFERENCE: 44921-5089-US
;  CURRENT APPLICATION NUMBER: US/10/152,319A
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: US 60/292,335
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/297,523
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,925
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,810
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,807
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,808
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/315,047
;  PRIOR FILING DATE: 2001-08-28
;  PRIOR APPLICATION NUMBER: US 60/324,928
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US 60/330,867
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/330,462
;  PRIOR FILING DATE: 2001-10-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2221
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1840
;   LENGTH: 4878
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. NM_024400
US-10-152-319A-1840

Alignment Scores:
Pred. No.:                0              Length:          4878
Score:                    4292.00        Matches:         789
Percent Similarity:       88.40%         Conservative:    57
Best Local Similarity:    82.45%         Mismatches:      97
Query Match:              82.71%         Indels:          14
DB:                       12             Gaps:            5

US-09-373-658C-2 (1-950) x US-10-152-319A-1840 (1-4878)

Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
              ||||||:::   :::||||||         ||||||                      ||||||
Db        446 ATGGGGGACATCCAGCGGGCAGCGAAGTTTCGGAGCTCTCAGTCTGCACACATGCTGTTG 505

Qy         21 LeuLeuAlaAlaAla---------LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37
              ||||||   |||:::         ||||||  |||       |||  ||||||||:::
Db        506 CTACTCCTCGCTTCCATAACAATGCTGCTGTGTGTGCGGGGCGCACACGGGCGCCCCACG 565

Qy         38 GluGluAspGluGluLeuValValProGluLeuGluArgAlaProGlyHis---GlyThr 56
              ||||||||||||||||||||:::|||  ||||||||||||  ||||||     |||
Db        566 GAGGAAGACGAGGAGCTGGTGCTGCCCTCGCTGGAGCGCGCCCGGGGCCACGATTCCACC 625

Qy         57 ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSer 76
              |||  |||||||||  ||||||  |||||||||  |||:::|||:::||||||||||
Db        626 ACACTCCTCCGTCTGGACGCCTTTGGTCAGCAGCTGCATCTGAAGTTGCAGCCAGACAGC 685

Qy         77 SerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThr 96
              ||||||||||||||||||||||||  |||||||||  |||||||||
Db        686 GGTTTCTTAGCGCCTGGCTTCACCCTCCAGACGGTGGGGCGCAGTCCTGGGTCCGAGGCA 745

Qy         97 ProLeu------ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGly 114
                  |||      ||||||||||||||||||||||||||||||||||||||||||||
Db        746 CAGCATCTGGACCCCACTGGGGACCTGGCCCACTGCTTCTACTCTGGCACGGTGAACGGT 805

Qy        115 AspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeu 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 GACCCCAGCTCCGCCGCCGCCCTCAGCCTCTGTGAAGGTGTGCGCGGTGCCTTCTACCTA 865

Qy        135 LeuGlyGluAlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThr 153
              ||||||   :::||||||||||||  ||||||  |||:::|||||||||
Db        866 CAAGGCGAGGAGTTCTTCATTCAGCCAGCGCCTGCGGTGGCCACCGAGCGCCTGGTCCCC 925

Qy        154 AlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArg 173
              |||  |||  |||:::      ||||||   :::||||||:::|||||||||  |||
Db        926 GCCGAACCGAAGGAGGAGTCAATCGCACCTCCGCGGTTCCACATCCTGAGGCGAAGGCGG 985

Qy        174 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 193
              :::|||      |||      |||||||||:::|||:::|||      ||||||
Db        986 CGGGGCAGCGGCGGCGCAAAGTGCGGTGTCATGGACGAAGAGACCCTGCCAACC------ 1039

Qy        194 AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer 213
                        :::  |||  |||  ::::::      ||||||
Db       1040 --------------AGCAACTCGGGTCGCGAAAGCCAGAACACCCCGGACCAGTGGCCT 1084

Qy        214 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 233
              ::::::|||      ||||||   |||:::||||||||   ||||||||||||||||
Db       1085 CTGCGGAACCCCACTCCTCAGGGCGCGGGAAAGCCAACAGGACCAGGAAGCATAAGGAAG 1144

Qy        234 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 253
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1145 AAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTGGCTGACCAGTCCATG 1204

Qy        254 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 273
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 GCTGACTTCCACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTCTCGGTGGCAGCC 1264

Qy        274 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeu 293
              |||  ||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db       1265 AGATTTTACAAGCACCCCAGCATTAGGAATTCAATTAGTCTGGTGGTGGTGAAGATCTTG 1324

Qy        294 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 313
              ||||||::::::||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 GTCATATATGAGGAGCAGAAGGGACCGGAAGTTACTTCCAATGCCGCTCTCACCCTTAGG 1384

Qy        314 AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 333
              ||||||||:::||||||||||||||||||  ||||||||||||||  |||||||||
Db       1385 AATTTCTGTAGCTGGCAGAAACAGCACAACAGCCCCAGTGACCGGGATCCAGAGCACTAT 1444

Qy        334 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 353
              ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       1445 GACACAGCGATTCTGTTCACCAGACAGGATTTATGTGGCTCCCACACCTGTGACACTCTC 1504

Qy        354 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1505 GGGATGGCTGATGTTGGAACTGTATGTGACCCCAGCAGGAGCTGTTCGGTCATCGAAGAT 1564

Qy        374 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 GATGGTTTACAGGCTGCCTTCACCACAGCCCATGAATTGGGCCATGTGTTTAACATGCCA 1624

Qy        394 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 413
              |||||||||||||  ||||||||||  |||||||||:::  ||||||||:::|||
Db       1625 CACGATGACGCCAAGCACTGCGCCAGCTTTAATGGCGTGAGTGGGGATTCCCATCTGATG 1684

Qy        414 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMet 433
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db       1685 GCCTCGATGCTCTCCAGCTTGGACCACAGCCAGCCCTGGTCTCCTTGCAGTGCCTACATG 1744

Qy        434 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 453
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1745 GTCACATCATTCCTGGACAACGGCCATGGGGAATGTTTGATGGACAAGCCGCAGAACCCA 1804

Qy        454 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 473
              |||:::||||||  ||||||||||||||  ||||||||||||||||||||||||||||||
Db       1805 ATCAAGCTCCCATCTGATCTTCCCGGTACCTTGTACGATGCCAACCGCCAGTGTCAGTTT 1864

Qy        474 ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp 493
              ||||||||||||:::|||  ||||||||||||||||||||||||||||||||||||||||
Db       1865 ACCTTCGGGGAGGAATCCACGCACTGCCCTGATGCAGCCAGCACATGCAGTACCCTGTGG 1924

Qy        494 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProProTrpAlaAsp 513
```

```
Db       1925 TGCACTGGCACCTCCGGTGGCTTACTGGTGTGCCAAACAAAACACTTCCCTTGGGCAGAT 1984

Qy        514 GlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThrAsp 533

Db       1985 GGCACCAGCTGCGGAGAAGGGAAATGGTGTGTCAGCGGCAAGTGTGTGAACAAGACCGAC 2044

Qy        534 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 553

Db       2045 ATGAAGCACTTTGCTACTCCTGTTCATGGGAGCTGGGGACCGTGGGGACCATGGGGAGAC 2104

Qy        554 CysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 573

Db       2105 TGCTCAAGAACCTGTGGTGGAGGAGTTCAATATACAATGAGAGAATGTGACAACCCGGTC 2164

Qy        574 ProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 593

Db       2165 CCAAAGAACGGGGGGAAGTACTGCGAAGGCAAACGAGTCCGCTACAGGTCCTGTAACATT 2224

Qy        594 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsn 613

Db       2225 GAGGACTGTCCAGACAATAACGGAAAAACATTCAGAGAGGAGCAATGCGAGGCGCACAAT 2284

Qy        614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAla 633

Db       2285 GAGTTTTCCAAAGCTTCCTTTGGGAATGAACCCACGGTGGAATGGACACCCAAGTATGCT 2344

Qy        634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 653

Db       2345 GGCGTCTCGCCAAAGGACAGGTGCAAGCTTACCTGCGAAGCCAAAGGCATTGGCTACTTC 2404

Qy        654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673

Db       2405 TTTGTTTTACAGCCCAAGGTGGTAGATGGCACTCCCTGTAGTCCAGACTCTACTTCTGTC 2464

Qy        674 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 693

Db       2465 TGTGTGCAAGGACAGTGTGTGAAAGCTGGCTGTGATCGCATCATAGACTCCAAAAAGAAG 2524

Qy        694 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySer 713

Db       2525 TTCGATAAGTGTGGCGTTTGTGGAGGAAATGGCTCCACGTGCAAGAAAATATCAGGAACG 2584

Qy        714 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 733

Db       2585 GTCACTAGTACAAGACCTGGGTATCATGACATTGTCACAATTCCTGCTGGAGCCACCAAC 2644

Qy        734 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIle 753

Db       2645 ATTGAAGTGAAACATCGTAATCCAAGGGGATCCAGAAACAATGGCAGCTTTCTGGCTATT 2704

Qy        754 LysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGln 773

Db       2705 AGAGCTGCAGATGGTACCTATATTCTGAATGGAAACTTCACTCTGTCCACTCTAGAGCAA 2764

Qy        774 AspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArg 793

Db       2765 GACCTCACCTACAAAGGTACTGTCTTAAGATACAGTGGTTCCTCAGCAGCATTGGAAAGA 2824

Qy        794 IleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsn 813

Db       2825 ATCCGCAGCTTTAGTCCACTCAAAGAACCCCTGACCATCCAGGTTCTTATGGTGGGCCAT 2884

Qy        814 AlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPheAsn 833

Db       2885 GCTCTCCGACCCAAAATCAAGTACACCTATTTTATGAAGAAGAAGACGGAGCCCTTCAAC 2944

Qy        834 AlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCys 853

Db       2945 GCTATTCCCACATTTTCGGAGTGGGTGATTGAAGAGTGGGGGGAGTGCTCCAAGACATGT 3004

Qy        854 GluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSer 873

Db       3005 GGTTCCGGTTGGCAGAGGAGAGTGGTAGAGTGCAGAGACATTAATGGACACCCTGCTTCT 3064

Qy        874 GluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPro 893

Db       3065 GAATGTGCCAAAGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGACCTTCCTTGCCCA 3124

Qy        894 GlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLys 913

Db       3125 CGTTGGCAGGTGGGGGATTGGTCACCATGTTCTAAAACTTGTGGGAAGGGTTATAAGAAG 3184

Qy        914 ArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAspPro 933

Db       3185 AGAACCTTGAAATGTCTGTCCCATGATGGCGGTGTGTTATCAAATGAGAGCTGTGATCCT 3244

Qy        934 LeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950

Db       3245 TTGAAGAAACCAAAGCATTACATTGACTTTTGCATACTGACACAGTGCAGT 3295
```

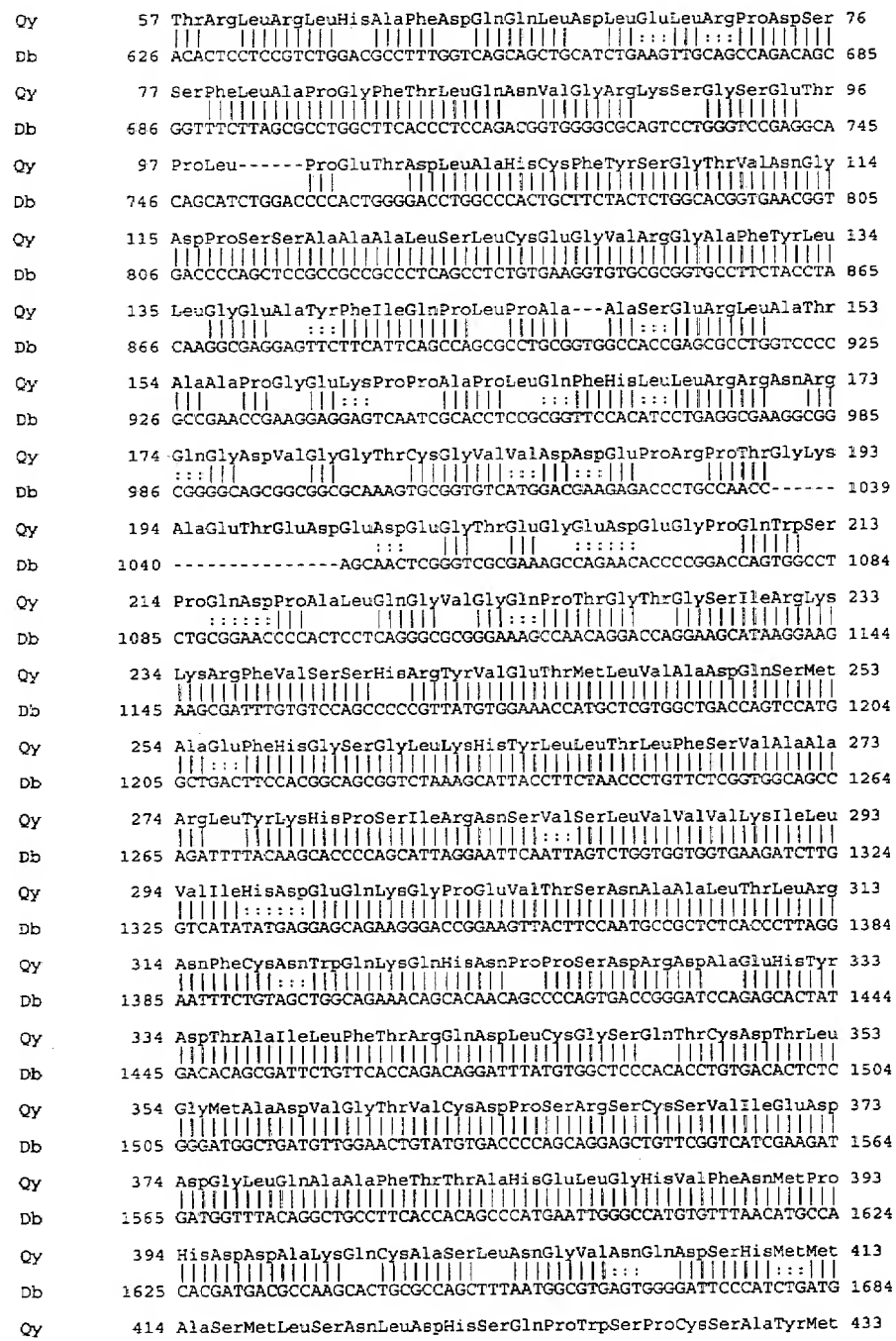
RESULT 14
US-10-191-803-170
; Sequence 170, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 170
; LENGTH: 4878
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_024400
US-10-191-803-170

Alignment Scores:

Pred. No.:	0	Length:	4878
Score:	4292.00	Matches:	789
Percent Similarity:	88.40%	Conservative:	57
Best Local Similarity:	82.45%	Mismatches:	97
Query Match:	82.71%	Indels:	14
DB:	16	Gaps:	5

US-09-373-658C-2 (1-950) x US-10-191-803-170 (1-4878)

```
Qy          1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20

Db        446 ATGGGGGACATCCAGCGGGCAGCGAAGTTTCGGAGCTCTCAGTCTGCACACATGCTGTTG 505

Qy         21 LeuLeuAlaAlaAla---------LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37

Db        506 CTACTCCTCGCTTCCATAACAATGCTGCTGTGTGTGCGGGGCGCACACGGGCGCCCCACG 565

Qy         38 GluGluAspGluGluLeuValValProGluLeuGluArgAlaProGlyHis---GlyThr 56

Db        566 GAGGAAGACGAGGAGCTGGTGCTGCCCTCGCTGGAGCGCGCCCGGGGCCACGATTCCACC 625
```


Qy 57 ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSer 76
Db 626 ACACTCCTCCGTCTGGACGCCTTTGGTCAGCAGCTGCATCTGAAGTTGCAGCCAGACAGC 685
Qy 77 SerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThr 96
Db 686 GGTTTCTTAGCGCCTGGCTTCACCCTCCAGACGGTGGGGCGCAGTCCTGGGTCCGAGGCA 745
Qy 97 ProLeu------ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGly 114
Db 746 CAGCATCTGGACCCCACTGGGGACCTGGCCCACTGCTTCTACTCTGGCACGGTGAACGGT 805
Qy 115 AspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeu 134
Db 806 GACCCCAGCTCCGCCGCCGCCCTCAGCCTCTGTGAAGGTGTGCGCGGTGCCTTCTACCTA 865
Qy 135 LeuGlyGluAlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThr 153
Db 866 CAAGGCGAGGAGTTCTTCATTCAGCCAGCGCCTGCGGTGGCCACCGAGCGCCTGGTCCCC 925
Qy 154 AlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArg 173
Db 926 GCCGAACCGAAGGAGGAGTCAATCGCACCTCCGCGGTTCCACATCCTGAGGCGAAGGCGG 985
Qy 174 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 193
Db 986 CGGGGCAGCGGCGGCGCAAAGTGCGGTGTCATGGACGAAGAGACCCTGCCAACC------ 1039
Qy 194 AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer 213
Db 1040 --------------AGCAACTCGGGTCGCGAAAGCCAGAACACCCCGGACCAGTGGCCT 1084
Qy 214 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 233
Db 1085 CTGCGGAACCCCACTCCTCAGGGCGCGGGAAAGCCAACAGGACCAGGAAGCATAAGGAAG 1144
Qy 234 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 253
Db 1145 AAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTGGCTGACCAGTCCATG 1204
Qy 254 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 273
Db 1205 GCTGACTTCCACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTCTCGGTGGCAGCC 1264
Qy 274 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeu 293
Db 1265 AGATTTTACAAGCACCCCAGCATTAGGAATTCAATTAGTCTGGTGGTGGTGAAGATCTTG 1324
Qy 294 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 313
Db 1325 GTCATATATGAGGAGCAGAAGGGACCGGAAGTTACTTCCAATGCCGCTCTCACCCTTAGG 1384
Qy 314 AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 333
Db 1385 AATTTCTGTAGCTGGCAGAAACAGCACAACAGCCCCAGTGACCGGGATCCAGAGCACTAT 1444
Qy 334 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 353
Db 1445 GACACAGCGATTCTGTTCACCAGACAGGATTTATGTGGCTCCCACACCTGTGACACTCTC 1504
Qy 354 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 373
Db 1505 GGGATGGCTGATGTTGGAACTGTATGTGACCCCAGCAGGAGCTGTTCGGTCATCGAAGAT 1564
Qy 374 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 393
Db 1565 GATGGTTTACAGGCTGCCTTCACCACAGCCCATGAATTGGGCCATGTGTTTAACATGCCA 1624
Qy 394 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 413
Db 1625 CACGATGACGCCAAGCACTGCGCCAGCTTTAATGGCGTGAGTGGGGATTCCCATCTGATG 1684
Qy 414 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMet 433
Db 1685 GCCTCGATGCTCTCCAGCTTGGACCACAGCCAGCCCTGGTCTCCTTGCAGTGCCTACATG 1744
Qy 434 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 453
Db 1745 GTCACATCATTCCTGGACAACGGCCATGGGGAATGTTTGATGGACAAGCCGCAGAACCCA 1804
Qy 454 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 473
Db 1805 ATCAAGCTCCCATCTGATCTTCCCGGTACCTTGTACGATGCCAACCGCCAGTGTCAGTTT 1864
Qy 474 ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp 493
Db 1865 ACCTTCGGGGAGGAATCCACGCACTGCCCTGATGCAGCCAGCACATGCAGTACCCTGTGG 1924
Qy 494 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProTrpAlaAsp 513
Db 1925 TGCACTGGCACCTCCGGTGGCTTACTGGTGTGCCAAACAAAACACTTCCCTTGGGCAGAT 1984
Qy 514 GlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThrAsp 533
Db 1985 GGCACCAGCTGCGGAGAAGGGAAATGGTGTGTCAGCGGCAAGTGTGTGAACAAGACCGAC 2044
Qy 534 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 553
Db 2045 ATGAAGCACTTTGCTACTCCTGTTCATGGGAGCTGGGGACCGTGGGGACCATGGGGAGAC 2104
Qy 554 CysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 573
Db 2105 TGCTCAAGAACCTGTGGTGGAGGAGTTCAATATACAATGAGAGAATGTGACAACCCGGTC 2164
Qy 574 ProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 593
Db 2165 CCAAAGAACGGGGGGAAGTACTGCGAAGGCAAACGAGTCCGCTACAGGTCCTGTAACATT 2224
Qy 594 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsn 613
Db 2225 GAGGACTGTCCAGACAATAACGGAAAAACATTCAGAGAGGAGCAATGCGAGGCGCACAAT 2284
Qy 614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAla 633
Db 2285 GAGTTTTCCAAAGCTTCCTTTGGGAATGAACCCACGGTGGAATGGACACCCAAGTATGCT 2344
Qy 634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 653
Db 2345 GGCGTCTCGCCAAAGGACAGGTGCAAGCTTACCTGCGAAGCCAAAGGCATTGGCTACTTC 2404
Qy 654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673
Db 2405 TTTGTTTTACAGCCCAAGGTGGTAGATGGCACTCCCTGTAGTCCAGACTCTACTTCTGTC 2464
Qy 674 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 693
Db 2465 TGTGTGCAAGGACAGTGTGTGAAAGCTGGCTGTGATCGCATCATAGACTCCAAAAAGAAG 2524
Qy 694 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySer 713
Db 2525 TTCGATAAGTGTGGCGTTTGTGGAGGAAATGGCTCCACGTGCAAGAAAATATCAGGAACG 2584
Qy 714 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 733
Db 2585 GTCACTAGTACAAGACCTGGGTATCATGACATTGTCACAATTCCTGCTGGAGCCACCAAC 2644
Qy 734 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIle 753
Db 2645 ATTGAAGTGAAACATCGTAATCCAAGGGGATCCAGAAACAATGGCAGCTTTCTGGCTATT 2704
Qy 754 LysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGln 773
Db 2705 AGAGCTGCAGATGGTACCTATATTCTGAATGGAAACTTCACTCTGTCCACTCTAGAGCAA 2764
Qy 774 AspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArg 793

```
Db       2765 GACCTCACCTACAAAGGTACTGTCTTAAGATACAGTGGTTCCTCAGCAGCATTGGAAAGA 2824

Qy        794 IleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsn 813

Db       2825 ATCCGCAGCTTTAGTCCACTCAAAGAACCCCTGACCATCCAGGTTCTTATGGTGGGCCAT 2884

Qy        814 AlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPheAsn 833

Db       2885 GCTCTCCGACCCAAAATCAAGTACACCTATTTTATGAAGAAGAAGACGGAGCCCTTCAAC 2944

Qy        834 AlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCys 853

Db       2945 GCTATTCCCACATTTTCGGAGTGGGTGATTGAAGAGTGGGGGGAGTGCTCCAAGACATGT 3004

Qy        854 GluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSer 873

Db       3005 GGTTCCGGTTGGCAGAGGAGAGTGGTAGAGTGCAGAGACATTAATGGACACCCTGCTTCT 3064

Qy        874 GluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPro 893

Db       3065 GAATGTGCCAAAGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGACCTTCCTTGCCCA 3124

Qy        894 GlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLys 913

Db       3125 CGTTGGCAGGTGGGGGATTGGTCACCATGTTCTAAAACTTGTGGGAAGGGTTATAAGAAG 3184

Qy        914 ArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAspPro 933

Db       3185 AGAACCTTGAAATGTCTGTCCCATGATGGCGGTGTGTTATCAAATGAGAGCTGTGATCCT 3244

Qy        934 LeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950

Db       3245 TTGAAGAAACCAAAGCATTACATTGACTTTTGCATACTGACACAGTGCAGT 3295
```

RESULT 15
US-09-445-023A-2
; Sequence 2, Application US/09445023A
; Patent No. US20020119167A1
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-2

Alignment Scores:

Pred. No.:	0	Length:	2184
Score:	3947.00	Matches:	712
Percent Similarity:	99.44%	Conservative:	4
Best Local Similarity:	98.89%	Mismatches:	4
Query Match:	76.06%	Indels:	0
DB:	9	Gaps:	0

US-09-373-658C-2 (1-950) x US-09-445-023A-2 (1-2184)

```
Qy        231 IleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAsp 250

Db         22 CTTAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTTGTGGCAGAC 81

Qy        251 GlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSer 270

Db         82 CAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCATTACCTTCTCACGTTGTTTTCG 141

Qy        271 ValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVal 290

Db        142 GTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAATTCAGTTAGCCTGGTGGTGGTG 201

Qy        291 LysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeu 310

Db        202 AAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAAGTGACCTCCAATGCTGCCCTC 261

Qy        311 ThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAla 330

Db        262 ACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAACCCACCCAGTGACCGGGATGCA 321

Qy        331 GluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCys 350

Db        322 GAGCACTATGACACAGCAATTCTTTTCACCAGACAGGACTTGTGTGGGTCCCAGACATGT 381

Qy        351 AspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerVal 370

Db        382 GATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTC 441

Qy        371 IleGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPhe 390

Db        442 ATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCCCATGAATTAGGCCACGTGTTT 501

Qy        391 AsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSer 410

Db        502 AACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTTAATGGTGTGAACCAGGATTCC 561

Qy        411 HisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSer 430

Db        562 CACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGCCAGCCTTGGTCTCCTTGCAGT 621

Qy        431 AlaTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysPro 450

Db        622 GCCTACATGATTACATCATTTCTGGATAATGGTCATGGGGAATGTTTGATGGACAAGCCT 681

Qy        451 GlnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGln 470

Db        682 CAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACCTTGTACGATGCCAACCGGCAG 741

Qy        471 CysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSer 490

Db        742 TGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCCGATGCAGCCAGCACATGTAGC 801

Qy        491 ThrLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProPro 510

Db        802 ACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTGTGTCAAACCAAACACTTCCCG 861

Qy        511 TrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsn 530

Db        862 TGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGTATCAACGGCAAGTGTGTGAAC 921

Qy        531 LysThrAspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro 550

Db        922 AAAACCGACAGGAAGCATTTTGATACGCCTTTTCATGGAAGCTGGGGACCATGGGGACCG 981

Qy        551 TrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAsp 570

Db        982 TGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGAC 1041

Qy        571 AsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSer 590

Db       1042 AACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAGATCC 1101
```

```
Qy       591 CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGlu 610
Db      1102 TGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATGTGAA 1161

Qy       611 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIlePro 630
Db      1162 GCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGATTCCC 1221

Qy       631 LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle 650
Db      1222 AAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATT 1281

Qy       651 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 670
Db      1282 GGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTTGATGGTACTCCATGTAGCCCAGATTCC 1341

Qy       671 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSer 690
Db      1342 ACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGACTCC 1401

Qy       691 LysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIle 710
Db      1402 AAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAATGGATCTACTTGTAAAAAAATA 1461

Qy       711 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 730
Db      1462 TCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGATATCGTCACAATTCCAACTGGA 1521

Qy       731 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 750
Db      1522 GCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGCAGCTTT 1581

Qy       751 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 770
Db      1582 CTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAATGGTGACTACACTTTGTCCACC 1641

Qy       771 LeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 790
Db      1642 TTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGGTACAGCGGCTCCTCTGCGGCA 1701

Qy       791 LeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThr 810
Db      1702 TTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACT 1761

Qy       811 ValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGlu 830
Db      1762 GTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTACTTCGTAAAGAAGAAGAAGGAA 1821

Qy       831 SerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSer 850
Db      1822 TCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATTGAAGAGTGGGGCGAATGTTCT 1881

Qy       851 LysSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGln 870
Db      1882 AAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAG 1941

Qy       871 ProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHis 890
Db      1942 CCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGACCAT 2001

Qy       891 ProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGly 910
Db      2002 CCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAAGGGT 2061

Qy       911 TyrLysLysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSer 930
Db      2062 TACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGC 2121

Qy       931 CysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950
Db      2122 TGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTTTGCACACTGACACAGTGCAGT 2181
```

Search completed: June 18, 2004, 23:44:17
Job time : 1093.17 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 17:11:45 ; Search time 150.321 Seconds
(without alignments)
3569.936 Million cell updates/sec

Title: US-09-373-658C-126
Perfect score: 5287
Sequence: 1 MQRAVPEGFGRRKLGSDMGN.....CDPLKKPKHPIDFCTMAECS 967

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09373658/runat_18062004_135343_10318/app_query.fasta_1.2254
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09373658_@CGN_1_1_156_@runat_18062004_135343_10318 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5232	99.0	4676	4	US-09-130-491-1	Sequence 1, Appli
	2	5230	98.9	3889	4	US-09-568-559-1	Sequence 1, Appli
	3	5219	98.7	4858	4	US-09-392-184-1	Sequence 1, Appli
	4	4262	80.6	3706	4	US-09-484-970B-58	Sequence 58, Appl
	5	3922	74.2	2184	4	US-09-445-023A-2	Sequence 2, Appli
	6	3652	69.1	2184	4	US-09-445-023A-13	Sequence 13, Appl
	7	2271.5	43.0	3638	4	US-09-369-364A-8	Sequence 8, Appli
c	8	2165	40.9	3126	4	US-09-392-184-7	Sequence 7, Appli
	9	2156	40.8	4192	4	US-09-122-126B-1	Sequence 1, Appli
	10	2156	40.8	4192	4	US-09-634-286A-1	Sequence 1, Appli
	11	1926.5	36.4	3250	4	US-09-122-126B-14	Sequence 14, Appl
	12	1926.5	36.4	3250	4	US-09-634-286A-14	Sequence 14, Appl
	13	1909.5	36.1	3002	4	US-09-369-364A-1	Sequence 1, Appli
	14	1751.5	33.1	5804	4	US-09-369-364A-12	Sequence 12, Appl
	15	1613	30.5	2625	4	US-09-369-364A-14	Sequence 14, Appl
	16	1406	26.6	2114	4	US-09-130-491-7	Sequence 7, Appli
c	17	1333.5	25.2	5357	4	US-09-392-184-5	Sequence 5, Appli
	18	1278.5	24.2	3675	4	US-09-930-872-3	Sequence 3, Appli
	19	1278.5	24.2	4042	4	US-09-930-872-5	Sequence 5, Appli
	20	1217	23.0	3218	4	US-09-369-364A-6	Sequence 6, Appli
	21	1214.5	23.0	2727	4	US-09-963-791-1	Sequence 1, Appli
	22	1203	22.8	3885	4	US-09-369-364A-16	Sequence 16, Appl
	23	1151.5	21.8	2274	4	US-09-963-791-23	Sequence 23, Appl
	24	1112	21.0	6692	4	US-09-491-522-1	Sequence 1, Appli
	25	1096	20.7	4580	4	US-09-491-522-8	Sequence 8, Appli
	26	1066.5	20.2	3160	4	US-09-963-791-25	Sequence 25, Appl
	27	1040.5	19.7	1520	4	US-09-369-364A-3	Sequence 3, Appli
	28	1038.5	19.6	2848	4	US-09-369-364A-4	Sequence 4, Appli
	29	950.5	18.0	2450	4	US-09-491-522-2	Sequence 2, Appli
	30	949.5	18.0	2450	4	US-09-491-522-9	Sequence 9, Appli
	31	781	14.8	1770	4	US-09-963-791-11	Sequence 11, Appl
	32	718	13.6	1317	4	US-09-963-791-21	Sequence 21, Appl
	33	712.5	13.5	739	4	US-09-369-364A-10	Sequence 10, Appl
c	34	639	12.1	1810	4	US-09-833-381-1056	Sequence 1056, Ap
	35	607.5	11.5	703	4	US-09-392-184-6	Sequence 6, Appli
	36	595	11.3	5720	4	US-09-800-729-18	Sequence 18, Appl
	37	593.5	11.2	1524	4	US-09-963-791-9	Sequence 9, Appli
	38	568.5	10.8	1803	4	US-09-369-364A-20	Sequence 20, Appl
	39	530.5	10.0	1071	4	US-09-963-791-19	Sequence 19, Appl
	40	499	9.4	1407	4	US-09-963-791-5	Sequence 5, Appli
	41	492	9.3	2023	4	US-09-491-522-6	Sequence 6, Appli
	42	477	9.0	1476	4	US-09-930-872-1	Sequence 1, Appli
	43	439	8.3	852	4	US-09-800-729-54	Sequence 54, Appl
	44	436	8.2	954	4	US-09-963-791-15	Sequence 15, Appl
	45	433	8.2	3559	4	US-09-800-729-53	Sequence 53, Appl

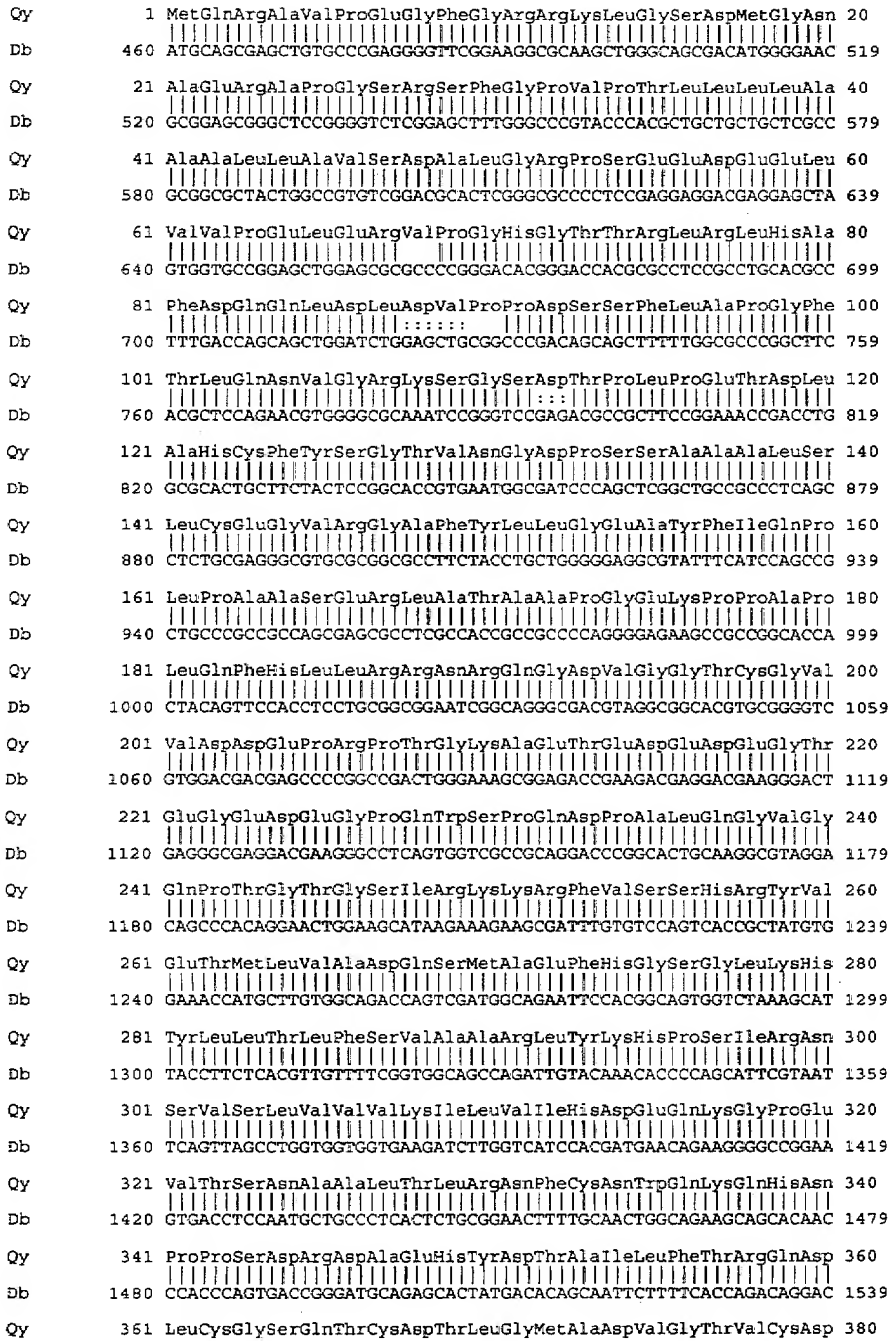
ALIGNMENTS

RESULT 1
US-09-130-491-1
; Sequence 1, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-09-130-491-1

Alignment Scores:

Pred. No.:	0	Length:	4676
Score:	5232.00	Matches:	957
Percent Similarity:	99.38%	Conservative:	4
Best Local Similarity:	98.97%	Mismatches:	6
Query Match:	98.96%	Indels:	0
DB:	4	Gaps:	0

US-09-373-658C-126 (1-967) x US-09-130-491-1 (1-4676)


Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 460 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 519
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db 520 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 579
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db 580 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 639
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 640 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 699
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 700 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 759
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 760 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 819
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db 820 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 879
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 880 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 939
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 940 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 999
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 1000 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACGTGCGGGGTC 1059
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1060 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 1119
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1120 GAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 1179
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 1180 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1239
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1240 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1299
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1300 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1359
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1360 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1419
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1420 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1479
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1480 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1539
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1540 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1599
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1600 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1659
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1660 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1719
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1720 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1779
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1780 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1839
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1840 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1899
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1900 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1959
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1960 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 2019
Qy 521 CysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 2020 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 2079
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 2080 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGGA 2139
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
Db 2140 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 2199
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 2200 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 2259
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 2260 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 2319
Qy 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2320 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2379
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2380 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2439
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2440 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2499
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 2500 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2559
Qy 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2560 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2619
Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740

```
Db       2620 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2679

Qy        741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2680 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2739

Qy        761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2740 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2799

Qy        781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2800 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2859

Qy        801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2860 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2919

Qy        821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2920 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2979

Qy        841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2980 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 3039

Qy        861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3040 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 3099

Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3100 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 3159

Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3160 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 3219

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3220 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 3279

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db       3280 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 3339

Qy        961 CysThrMetAlaGluCysSer 967
              |||||||||||||||||||||
Db       3340 TGCACAATGGCAGAATGCAGT 3360
```

RESULT 2
US-09-568-559-1
; Sequence 1, Application US/09568559
; Patent No. 6549377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-09-568-559-1

Alignment Scores:

Pred. No.:	0	Length:	3889
Score:	5230.00	Matches:	956
Percent Similarity:	99.38%	Conservative:	5
Best Local Similarity:	98.86%	Mismatches:	6
Query Match:	98.92%	Indels:	0
DB:	4	Gaps:	0

US-09-373-658C-126 (1-967) x US-09-568-559-1 (1-3889)

```
Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 ATGCAGCGATCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 67

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTCTCGCC 127

Qy         41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 187

Qy         61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 247

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
              ||||||||||||||||||||||:::::: ||||||||||||||||||||||||||||||
Db        248 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 307

Qy        101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
              ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db        308 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 367

Qy        121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 427

Qy        141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 487

Qy        161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 547

Qy        181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACGTGCGGGGTC 607

Qy        201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 667

Qy        221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        668 GAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 727

Qy        241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 787

Qy        261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 847

Qy        281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 907

Qy        301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        908 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 967
Qy        321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db        968 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1027
Qy        341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db       1028 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1087
Qy        361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db       1088 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1147
Qy        381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db       1148 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1207
Qy        401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db       1208 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1267
Qy        421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db       1268 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1327
Qy        441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db       1328 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1387
Qy        461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db       1388 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1447
Qy        481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db       1448 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCT 1507
Qy        501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db       1508 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 1567
Qy        521 CysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db       1568 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 1627
Qy        541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db       1628 ATCAACGGCAAGTGTGTGAACAAAACCCACAGAAAGCATTTTGATACGCCTTTTCATGGA 1687
Qy        561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
Db       1688 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 1747
Qy        581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db       1748 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 1807
Qy        601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db       1808 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 1867
Qy        621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db       1868 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 1927
Qy        641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db       1928 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 1987
Qy        661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db       1988 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2047

Qy        681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db       2048 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2107
Qy        701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db       2108 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2167
Qy        721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db       2168 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2227
Qy        741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db       2228 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2287
Qy        761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db       2288 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2347
Qy        781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db       2348 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2407
Qy        801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db       2408 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2467
Qy        821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db       2468 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2527
Qy        841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db       2528 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 2587
Qy        861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db       2588 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 2647
Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db       2648 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 2707
Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db       2708 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 2767
Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db       2768 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 2827
Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db       2828 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 2887
Qy        961 CysThrMetAlaGluCysSer 967
Db       2888 TGCACAATGGCAGAATGCAGT 2908
```

RESULT 3
US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33

```
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 4858
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(4858)
;   OTHER INFORMATION: reprolysin (ADAM family of metalloprotease)
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(4858)
;   OTHER INFORMATION: n = A,T,C or G
US-09-392-184-1

Alignment Scores:
Pred. No.:                0                Length:          4858
Score:                    5219.00          Matches:         957
Percent Similarity:       99.28%           Conservative:    4
Best Local Similarity:    98.86%           Mismatches:      6
Query Match:              98.71%           Indels:          1
DB:                       4                Gaps:            0

US-09-373-658C-126 (1-967) x US-09-392-184-1 (1-4858)

Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 513

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 573

Qy         41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 633

Qy         61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
              ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 693

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
              ||||||||||||||||||::::::  ||||||||||||||||||||||||||||||||||||
Db        694 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 753

Qy        101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
              ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db        754 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 813

Qy        121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 873

Qy        141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 933

Qy        161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 993

Qy        181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACGTGCGGGGTC 1053

Qy        201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 1113

Qy        221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 GAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 1173

Qy        241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1233

Qy        261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1293

Qy        281 TyrLeuLeu-ThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAs 300
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 TACCTTCTCAACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAA 1353

Qy        300 nSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGl 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGA 1413

Qy        320 uValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAs 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 AGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAA 1473

Qy        340 nProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAs 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 CCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGA 1533

Qy        360 pLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAs 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGA 1593

Qy        380 pProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAl 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGC 1653

Qy        400 aHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLe 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 CCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCT 1713

Qy        420 uAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSe 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 TAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAG 1773

Qy        440 rGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGl 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGG 1833

Qy        460 yGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyTh 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCAC 1893

Qy        480 rSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCC 1953

Qy        500 oAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVa 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 TGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGT 2013

Qy        520 lCysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCy 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 GTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTG 2073

Qy        540 sIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGl 560
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       2074 TATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGG 2133

Qy        560 ySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGl 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 AAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCA 2193

Qy        580 nTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGl 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 GTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGG 2253

Qy        600 yLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysTh 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       2254 CAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAAC 2313

Qy        620 rPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGl 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 CTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGG 2373

Qy        640 yProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLe 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 GCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCT 2433

Qy        660 uIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGl 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 CATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGG 2493

Qy        680 yThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGl 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 TACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGG 2553

Qy        700 yCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAs 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 TTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAA 2613

Qy        720 nGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAs 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 TGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGA 2673

Qy        740 pIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGl 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 TATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGG 2733

Qy        760 ySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAs 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 ATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAA 2793

Qy        780 nGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuAr 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 TGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAG 2853

Qy        800 gTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPr 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 GTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCC 2913

Qy        820 oLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTy 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 CTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTA 2973

Qy        840 rPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIl 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2974 CTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAT 3033

Qy        860 eGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGl 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 TGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGA 3093

Qy        880 uCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSe 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAG 3153

Qy        900 rThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCy 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 CACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATG 3213

Qy        920 sSerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGl 940
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db       3214 TTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGG 3273

Qy        940 yGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPh 960
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTT 3333

Qy        960 eCysThrMetAlaGluCysSer 967
              |||||||||||||||||||||
Db       3334 TTGCACAATGGCAGAATGCAGT 3355
```

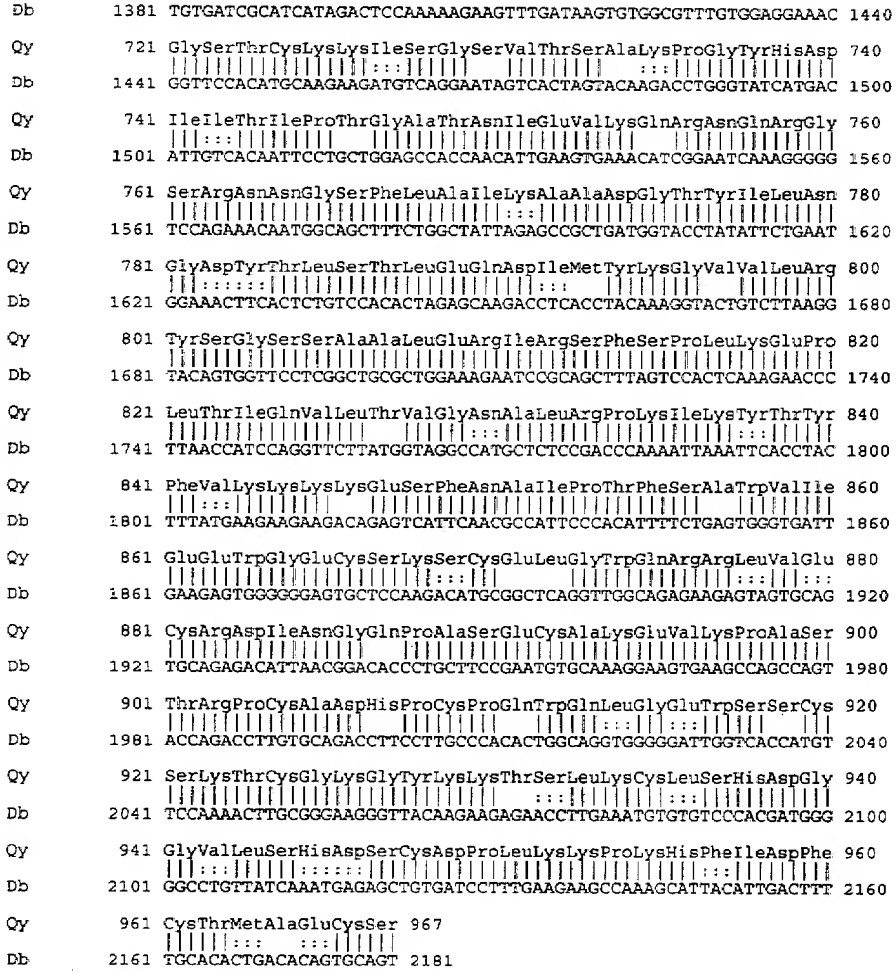
```
RESULT 4
US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;  APPLICANT:  Jones, Karen A.
;  APPLICANT:  Volkmuth, Wayne
;  APPLICANT:  Walker, Michael G.
;  TITLE OF INVENTION:  BONE REMODELING GENES
;  FILE REFERENCE:  PB-0014 US
;  CURRENT APPLICATION NUMBER: US/09/484,970B
;  CURRENT FILING DATE:  2000-01-18
;  NUMBER OF SEQ ID NOS:  172
;  SOFTWARE:  PERL Program
; SEQ ID NO 58
;   LENGTH: 3706
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6426186 007074.1
;   NAME/KEY: unsure
;   LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
;   OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Alignment Scores:
Pred. No.:                0                Length:          3706
Score:                    4262.00          Matches:         772
Percent Similarity:       99.36%           Conservative:    1
Best Local Similarity:    99.23%           Mismatches:      4
Query Match:              80.61%           Indels:          1
DB:                       4                Gaps:            0

US-09-373-658C-126 (1-967) x US-09-484-970B-58 (1-3706)

Qy        191 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CAGGGCGACGTAGGCGGCACGTGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAA 62

Qy        211 AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCGGAGACCGAAGACGAGGACGAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCG 122

Qy        231 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCGCAGGACCCGGCACTGCAAGGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAG 182

Qy        251 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AAGCGATTTGTGTCCAGTCACCGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATG 242

Qy        271 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GCAGAATTCCACGGCAGTGGTCTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCC 302

Qy        291 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeu 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 AGATTGTACAAACACCCCAGCATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTG 362

Qy        311 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCATCCACGATGAACAGAAGGGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGG 422

Qy        331 AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTTTTGCAACTGGCAGAAGCAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTAT 482

Qy        351 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GACACAGCAATTCTTTTCACCAGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTT 542
```

```
Qy      371 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 390
Db      543 GGGATGGCTGATGTTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGAT 602

Qy      391 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 410
Db      603 GATGGTTTACAAGCTGCCTTCACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCA 662

Qy      411 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 430
Db      663 CATGATGATGCAAAGCAGTGTGCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATG 722

Qy      431 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMet 450
Db      723 GCGTCAATGCTTTCCAACCTGGACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATG 782

Qy      451 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 470
Db      783 ATTACATCATTTCTGGATAATGGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCC 842

Qy      471 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 490
Db      843 ATACAGCTCCCAGGCGATCTCCCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTT 902

Qy      491 ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp 510
Db      903 ACATTTGGGGAGGACTCCAAACACTGCCCCGATGCAGCCAGCACATGTAGCACCTTGTGG 962

Qy      511 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisProProTrpAlaAsp 530
Db      963 TGTACCGGCACCTCTGGTGGGGTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGAT 1022

Qy      531 GlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHis 550
Db     1023 GGCACCAGCTGTGGAGAAGGGAAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGAC 1082

Qy      551 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 570
Db     1083 AGAAAGCATTTTGATACGCCTTTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGAC 1142

Qy      571 CysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 590
Db     1143 TGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTC 1202

Qy      591 ProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 610
Db     1203 CCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTT 1262

Qy      611 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsn 630
Db     1263 GAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAAC 1322

Qy      631 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAla 650
Db     1323 GAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCT 1382

Qy      651 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 670
Db     1383 GGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTC 1442

Qy      671 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 690
Db     1443 TTCGTTTTGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTC 1502

Qy      691 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 710
Db     1503 TGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAG 1562

Qy      711 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySer 730
Db     1563 TTTGATAAATGTGGTGTTTGCGGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCA 1622

Qy      731 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 750

Db     1623 GTTACTAGTGCAAAACCTGGATATCATGATATCATCACAATTCCAACTGGAGCCACCAAC 1682

Qy      751 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIl 770
Db     1683 ATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGGCAGCTTTCTTGCCAT 1742

Qy      770 eLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGl 790
Db     1743 CAAAGCTGCTGATGGCACATATATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCA 1802

Qy      790 nAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluAr 810
Db     1803 AGACATTATGTACAAAGGTGTTGTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAG 1862

Qy      810 gIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 830
Db     1863 AATTCGCAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAA 1922

Qy      830 nAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGluSerPheAs 850
Db     1923 TGCCCTTCGACCTAAAATTAAATACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAA 1982

Qy      850 nAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCy 870
Db     1983 TGCTATCCCCACTTTTTCAGCATGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATG 2042

Qy      870 sGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSe 890
Db     2043 TGAATTGGGTTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTC 2102

Qy      890 rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 910
Db     2103 CGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCC 2162

Qy      910 oGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLy 930
Db     2163 CCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAA 2222

Qy      930 sThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSerCysAspPr 950
Db     2223 AAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCC 2282

Qy      950 oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
Db     2283 TTTAAAGAAACCTAAACATTTCATAGACTTTTGCACAATGGCAGAATGCAGT 2334
```

RESULT 5
US-09-445-023A-2
; Sequence 2, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```
;   NAME/KEY: exon
;   LOCATION: (1)..(2184)
US-09-445-023A-2

Alignment Scores:
Pred. No.:                0              Length:          2184
Score:                    3922.00        Matches:         707
Percent Similarity:       98.89%         Conservative:    5
Best Local Similarity:    98.19%         Mismatches:      8
Query Match:              74.18%         Indels:          0
DB:                       4              Gaps:            0

US-09-373-658C-126 (1-967) x US-09-445-023A-2 (1-2184)

Qy        248 IleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAsp 267
              :::|||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db         22 CTTAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTTGTGGCAGAC  81

Qy        268 GlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSer 287
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCATTACCTTCTCACGTTGTTTTCG 141

Qy        288 ValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVal 307
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 GTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAATTCAGTTAGCCTGGTGGTGGTG 201

Qy        308 LysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeu 327
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAAGTGACCTCCAATGCTGCCCTC 261

Qy        328 ThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAla 347
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 ACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAACCCACCCAGTGACCGGGATGCA 321

Qy        348 GluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCys 367
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 GAGCACTATGACACAGCAATTCTTTTCACCAGACAGGACTTGTGTGGGTCCCAGACATGT 381

Qy        368 AspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerVal 387
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTC 441

Qy        388 IleGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPhe 407
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCCCATGAATTAGGCCACGTGTTT 501

Qy        408 AsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSer 427
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 AACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTTAATGGTGTGAACCAGGATTCC 561

Qy        428 HisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSer 447
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGCCAGCCTTGGTCTCCTTGCAGT 621

Qy        448 GlyTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysPro 467
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 GCCTACATGATTACATCATTTCTGGATAATGGTCATGGGGAATGTTTGATGGACAAGCCT 681

Qy        468 GlnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGln 487
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACCTTGTACGATGCCAACCGGCAG 741

Qy        488 CysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSer 507
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCCGATGCAGCCAGCACATGTAGC 801

Qy        508 ThrLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPhePro 527
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 ACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTGTGTCAAACCAAACACTTCCCG 861

Qy        528 TrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsn 547
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGTATCAACGGCAAGTGTGTGAAC 921

Qy        548 LysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro 567
              |||  ||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        922 AAAACCGACAGGAAGCATTTTGATACGCCTTTTCATGGAAGCTGGGGACCATGGGGACCG 981

Qy        568 TrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAsp 587
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGAC 1041

Qy        588 AsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSer 607
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 AACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAGATCC 1101

Qy        608 CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGlu 627
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 TGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATGTGAA 1161

Qy        628 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIlePro 647
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 GCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGATTCCC 1221

Qy        648 LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle 667
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 AAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATT 1281

Qy        668 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 687
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 GGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTTGATGGTACTCCATGTAGCCCAGATTCC 1341

Qy        688 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSer 707
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 ACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGACTCC 1401

Qy        708 LysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIle 727
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db       1402 AAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAATGGATCTACTTGTAAAAAAATA 1461

Qy        728 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 747
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 TCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGATATCGTCACAATTCCAACTGGA 1521

Qy        748 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 767
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 GCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGCAGCTTT 1581

Qy        768 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 787
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1582 CTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAATGGTGACTACACTTTGTCCACC 1641

Qy        788 LeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 807
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1642 TTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGGTACAGCGGCTCCTCTGCGGCA 1701

Qy        808 LeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThr 827
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1702 TTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACT 1761

Qy        828 ValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGlu 847
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1762 GTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTACTTCGTAAAGAAGAAGAAGGAA 1821

Qy        848 SerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSer 867
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1822 TCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATTGAAGAGTGGGGCGAATGTTCT 1881

Qy        868 LysSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGln 887
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1882 AAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAG 1941

Qy        888 ProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHis 907
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1942 CCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGACCAT 2001
```

```
Qy        908 ProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGly 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2002 CCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAAGGGT 2061

Qy        928 TyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSer 947
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||:::|||
Db       2062 TACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGC 2121

Qy        948 CysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
              ||||||||||||||||||||||||||||||||||||||||||||||:::   :::||||||
Db       2122 TGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTTTGCACACTGACACAGTGCAGT 2181

RESULT 6
US-09-445-023A-13
; Sequence 13, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
;  APPLICANT: Hirose, Kunitaka
;  APPLICANT:  Inoguchi, Eiji
;  APPLICANT:  Hakozaki, Michinori
;  APPLICANT:  Ishioka, Keiko
;  APPLICANT:  Ishida, Yukako
;  APPLICANT:  Matsushima, Kouji
;  APPLICANT:  Kuno, Kouji
;  TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
;  TITLE OF INVENTION:  composition and method of immunologically analyzing human ADAMTS
;  FILE REFERENCE: Q57092
;  CURRENT APPLICATION NUMBER: US/09/445,023A
;  CURRENT FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER: JP 9-160422
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 2184
;   TYPE: DNA
;   ORGANISM: Mus sp.
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(2184)
US-09-445-023A-13

Alignment Scores:
Pred. No.:                0          Length:          2184
Score:                 3652.00       Matches:          646
Percent Similarity:     94.77%       Conservative:      43
Best Local Similarity:  88.86%       Mismatches:        38
Query Match:            69.08%       Indels:             0
DB:                     4            Gaps:               0

US-09-373-658C-126 (1-967) x US-09-445-023A-13 (1-2184)

Qy        241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
              :::|||:::|||  ||||||||||||||||||||||||||||||||||||  |||||||||
Db          1 AAGCCATCAGGACCAGGAAGCATAAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTG 60

Qy        261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db         61 GAAACCATGCTCGTAGCTGACCAGTCCATGGCCGACTTCCACGGCAGCGGTCTAAAGCAT 120

Qy        281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 TACCTTCTAACCCTGTTCTCGGTGGCAGCCAGGTTTTACAAGCATCCCAGCATTAGGAAT 180

Qy        301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
              |||:::|||||||||||||||||||||||||||||:::::|||||||||||||||||||
Db        181 TCAATTAGCCTGGTGGTGGTGAAGATCTTGGTCATATACGAGGAGCAGAAGGGACCAGAA 240

Qy        321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        241 GTTACCTCCAATGCAGCTCTCACCCTTCGGAATTTCTGCAGCTGGCAGAAACAACACAAC 300

Qy        341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCCCCAGTGACCGGGATCCAGAGCACTATGACACTGCAATTCTGTTCACCAGACAGGAT 360

Qy        361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
              ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTATGTGGCTCCCACACGTGTGACACTCTCGGAATGGCAGATGTTGGAACCGTATGTGAC 420

Qy        381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCAGCAGGAGCTGCTCAGTCATAGAAGATGATGGTTTGCAAGCTGCCTTCACCACAGCC 480

Qy        401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        481 CATGAATTGGGCCATGTGTTTAACATGCCGCACGATGATGCTAAGCACTGTGCCAGCTTG 540

Qy        421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
              |||||||||:::  ||||||||||:::||||||||||||||||||:::||||||||||||
Db        541 AATGGTGTGAGTGGCGATTCTCATCTGATGGCCTCGATGCTCTCCAGCTTAGACCATAGC 600

Qy        441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
              ||||||||||||||||||||  ||||||:::||||||||||||||||||||||||||||||
Db        601 CAGCCCTGGTCACCTTGCAGTGCCTACATGGTCACGTCCTTCCTAGATAATGGACACGGG 660

Qy        461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
              |||||||||||||||||||||||||||||||||||:::||||||  ||||||||||||||||
Db        661 GAATGTTTGATGGACAAGCCCCAGAATCCAATCAAGCTCCCTTCTGATCTTCCCGGTACC 720

Qy        481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        721 TTGTACGATGCCAACCGCCAGTGTCAGTTTACATTCGGAGAGGAATCCAAGCACTGCCCT 780

Qy        501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
              ||||||||||||||||||:::||||||||||||||||||||||||||||:::||||||||||
Db        781 GATGCAGCCAGCACATGTACTACCCTGTGGTGCACTGGCACCTCCGGTGGCTTACTGGTG 840

Qy        521 CysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGCCAAACAAAACACTTCCCTTGGGCAGATGGCACCAGCTGTGGAGAAGGGAAGTGGTGT 900

Qy        541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
              ::::::|||||||||||||||||||||||||||  ||||||||  ||||||  ||||||
Db        901 GTCAGTGGCAAGTGCGTGAACAAGACAGACATGAAGCATTTTGCTACTCCTGTTCATGGA 960

Qy        561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGGGGACCATGGGGACCGTGGGGAGACTGCTCAAGAACCTGTGGTGGTGGAGTTCAA 1020

Qy        581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACACAATGAGAGAATGTGACAACCCAGTCCCAAAGAACGGAGGGAAGTACTGTGAAGGC 1080

Qy        601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db       1081 AAACGAGTCCGCTACAGGTCCTGTAACATCGAGGACTGTCCAGACAATAACGGAAAAACG 1140

Qy        621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1141 TTCAGAGAGGAGCAGTGCGAGGCGCACAATGAGTTTTCCAAAGCTTCCTTTGGGAATGAG 1200

Qy        641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
              |||  ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCACTGTAGAGTGGACACCCAAGTACGCCGGCGTCTCGCCAAAGGACAGGTGCAAGCTC 1260

Qy        661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ACCTGTGAAGCCAAAGGCATTGGCTACTTTTTCGTCTTACAGCCCAAGGTTGTAGATGGC 1320

Qy        681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACTCCCTGTAGTCCAGACTCTACCTCTGTCTGTGTGCAAGGGCAGTGTGTGAAAGCTGGC 1380

Qy        701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

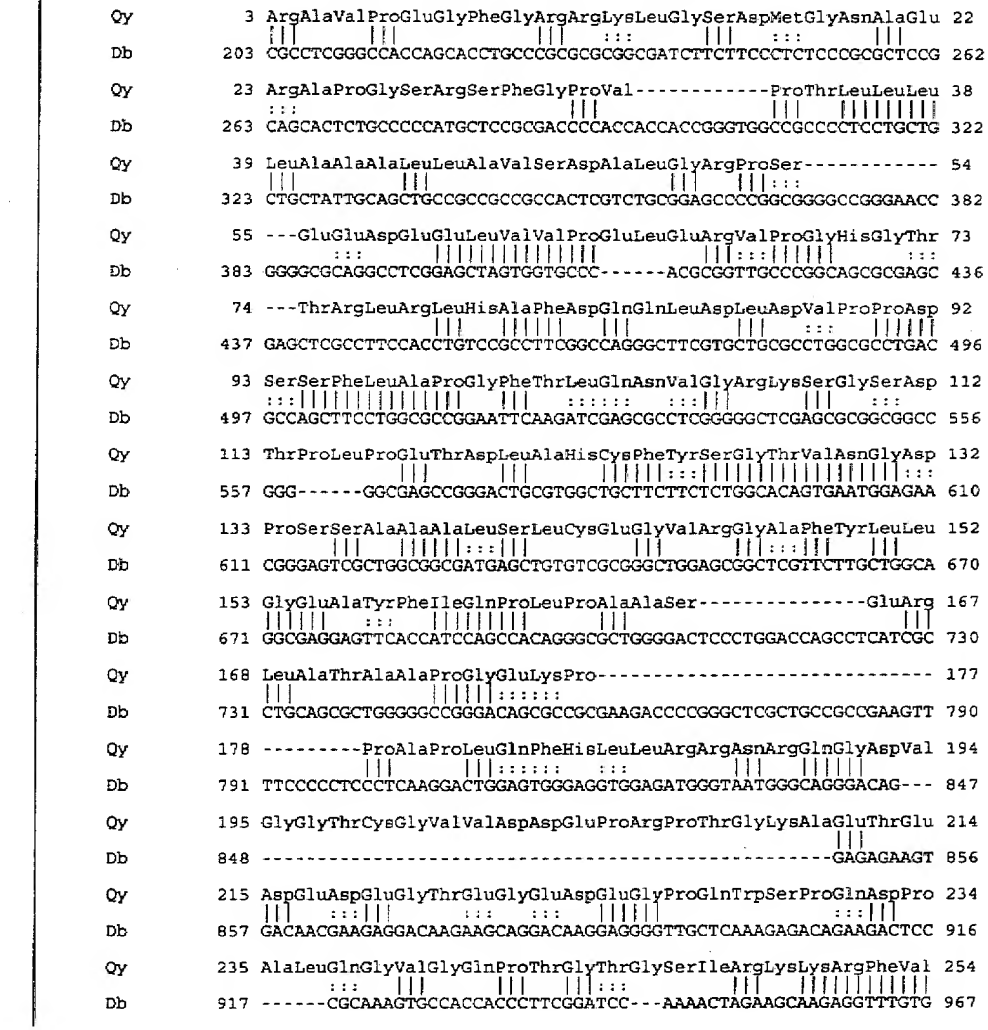


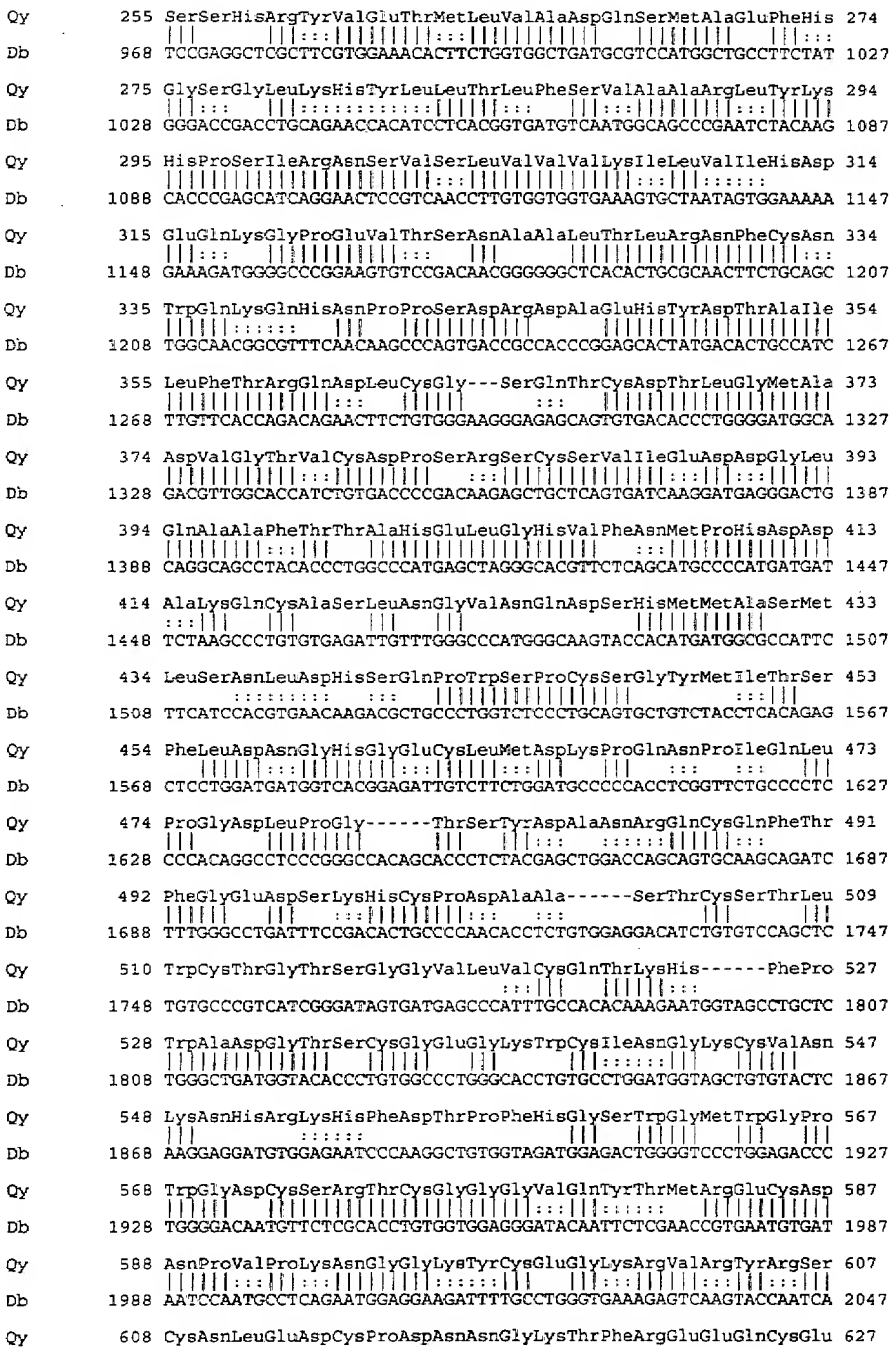
RESULT 7
US-09-369-364A-8
; Sequence 8, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3638
; TYPE: DNA
; ORGANISM: Mus musculus ADAMTS-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (278)..(2992)
; NAME/KEY: misc_feature
; LOCATION: (3636)
; OTHER INFORMATION: n = T
US-09-369-364A-8

Alignment Scores:

Pred. No.:	2.62e-195	Length:	3638
Score:	2271.50	Matches:	452
Percent Similarity:	61.66%	Conservative:	151
Best Local Similarity:	46.22%	Mismatches:	288
Query Match:	42.96%	Indels:	87
DB:	4	Gaps:	22

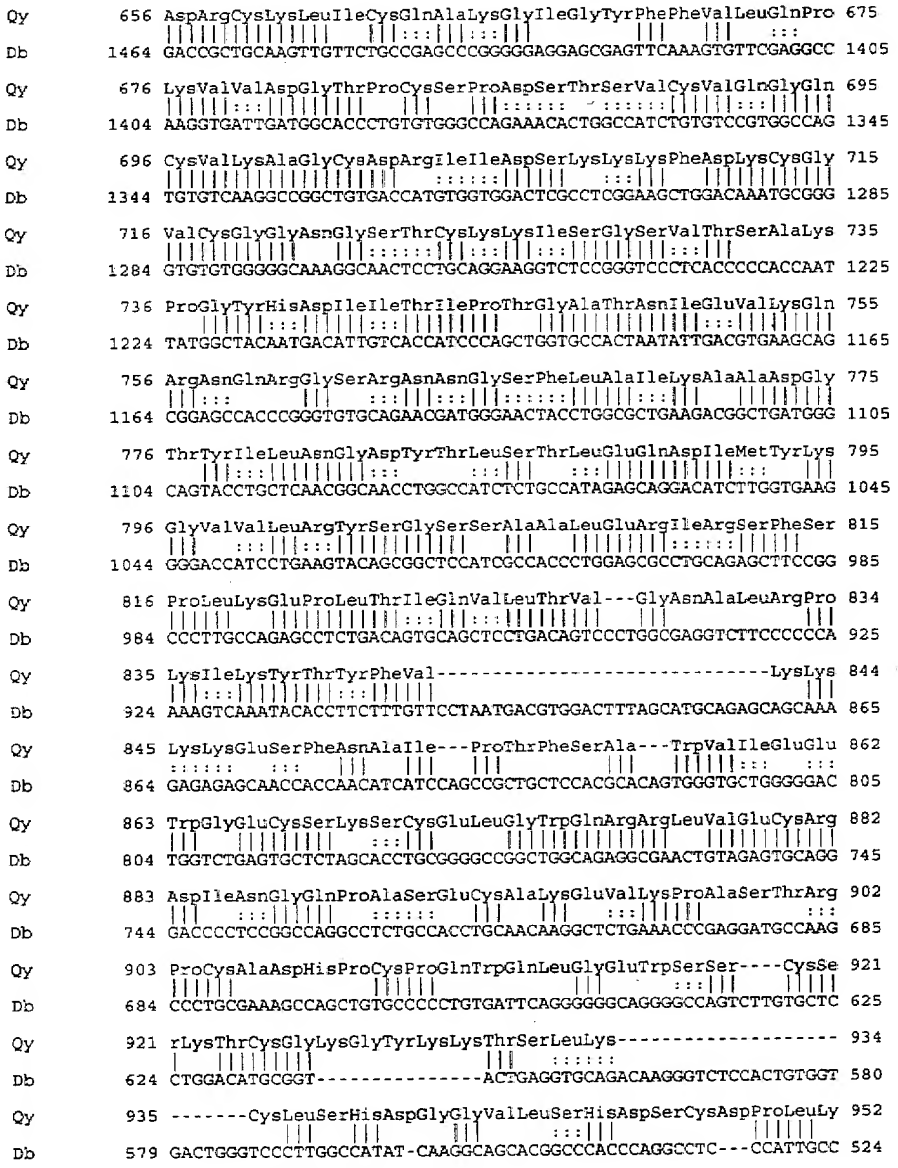
US-09-373-658C-126 (1-967) x US-09-369-364A-8 (1-3638)





RESULT 8
US-09-392-184-7/c
; Sequence 7, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.

```
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN
;  TITLE OF INVENTION:  PROTEASE HOMOLOGS
;  FILE REFERENCE:  5800-55
;  CURRENT APPLICATION NUMBER: US/09/392,184
;  CURRENT FILING DATE:  1999-09-09
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 3126
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3126)
;   OTHER INFORMATION: reprolysin (ADAM family of metalloprotease)
US-09-392-184-7

Alignment Scores:
Pred. No.:                9.05e-186       Length:          3126
Score:                    2165.00         Matches:         443
Percent Similarity:       62.49%          Conservative:    140
Best Local Similarity:    47.48%          Mismatches:      246
Query Match:              40.95%          Indels:          106
DB:                       4               Gaps:            24

US-09-373-658C-126 (1-967) x US-09-392-184-7 (1-3126)

Qy        76 LeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPhe 95
Db      3116 CTCCACCTGTCCGCCTTCGGCAAGGGCTTCGTGCTGCGCCTGGCGCCCGACGACAGCTTC 3057

Qy        96 LeuAlaProGlyPheThrLeuGlnAsnVal---------GlyArgLysSerGlySerAsp 112
Db      3056 CTGGCGCCCGACTTCAAGATCGAGCGCCTCGGGGGCTCCGGCCGGGCGACCGGGGGC--- 3000

Qy       113 ThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAsp 132
Db      2999 ------------GAGCGGGGGCTGCGCGGCTGCTTCTTCTCCGGCACCGTCCACGCGTCC 2952

Qy       133 ProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeu 152
Db      2951 GCCGAGTCGCTGGCGGCGGTCAGCCTGTGCCGCGGGCTGAGCGGCTCCTTCCTGCTGGAC 2892

Qy       153 GlyGluAlaTyrPheIleGlnProLeuProAlaAlaSer---------------GluArg 167
Db      2891 GGCGAGGAGTTCACCATCCAGCCGCAGGGCGCGGGGGGCTCCCTGGGTCAGCCGCACCGC 2832

Qy       168 LeuAlaThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArg 187
Db      2831 CTGCAGCGCTGGGGTCCCGC-CGGAGCCCGCCCCCTCCC-----------------GCG 2791

Qy       188 ArgAsnArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgPro 207
Db      2790 AGGACCCGAGTGGGAGGTGGAGACGGGAGA---GGGTCAGAGGCAGGAGAGAGGAGACCA 2734

Qy       208 ThrGly-LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyPr 227
Db      2733 CCAGGAGGACAGCGAGGAGGAGAGCCAAGAAGAGGAGGCAGAAGGCGCTAGCGAGCCGCC 2674

Qy       227 oGlnTrpSerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySe 247
Db      2673 A-----------------------------------CCGCCCCTGGGGGCCACGAG 2653

Qy       247 rIleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAs 267
Db      2652 T---AGGACCAAGCGGTTTGTGTCTGAGGCGCGCTTCGTGGAGACGCTGCTGGTGGCCGA 2596

Qy       267 pGlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSe 287
Db      2595 TGCGTCCATGGCTGCCTTCTACGGGGCCGACCTGCAGAACCACATCCTGACGTTAATGTC 2536

Qy       287 rValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVa 307
Db      2535 TGTGGCAGCCCGAATCTACAAGCACCCCAGCATCAAGAATTCCATCAACCTGATGGTGGT 2476

Qy       307 lLysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLe 327
Db      2475 AAAAGTGCTGATCGTAGAAGATGAAAAATGGGGCCCAGAGGTGTCCGACAATGGGGGGCT 2416

Qy       327 uThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAl 347
Db      2415 TACACTGCGTAACTTCTGCAACTGGCAGCGGCGTTTCAACCAGCCCAGCGACCGCCACCC 2356

Qy       347 aGluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGln---Th 366
Db      2355 AGAGCACTACGACACGGCCATCCTGCTCACCAGACAGAACTTCTGTGGGCAGGAGGGGCT 2296

Qy       366 rCysAspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSe 386
Db      2295 GTGTGACACCCTGGGTGTGGCAGACATCGGGACCATTTGTGACCCCAACAAAAGCTGCTC 2236

Qy       386 rValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisVa 406
Db      2235 CGTGATCGAGGATGAGGGGCTCCAGGCGGCCCACACCCTGGCCCATGAACTAGGGCACGT 2176

Qy       406 lPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAs 426
Db      2175 CCTCAGCATGCCCCACGACGACTCCAAGCCCTGCACACGGCTCTTCGGGCCCATGGGCAA 2116

Qy       426 pSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCy 446
Db      2115 GCACCACGTGATGGCACCGCTGTTCGTCCACCTGAACCAGACGCTGCCCTGGTCCCCCTG 2056

Qy       446 sSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHis----------------Gl 460
Db      2055 CAGCGCCATGTATCTCACAGAGCTTCTTGACGGGGGGCACCGATTTCAGGTATTTATGGC 1996

Qy       460 yGluCysLeu-MetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyT 480
Db      1995 CCTGTGTCTAGGTG---------------------------------------------- 1982

Qy       480 hrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysP 500
Db      1981 --------------CTACAGCGTTGCATTATGCTCTTTGGGCCGGATTTCCGCCACTGCC 1936

Qy       500 roAsp------AlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyV 518
Db      1935 CCAACACCTCTGCTCAGGACGTCTGCGCCCAGCTTTGGTGC---CACACTGATGGGGCTG 1879

Qy       518 alLeuValCysGlnThrLysHis------ProProTrpAlaAspGlyThrSerCysGlyG 536
Db      1878 AGCCCCTGTGCCACACGAAGAATGGCAGCCTGCCCTGGGCTGACGGCACGCCGTGCGGGC 1819

Qy       536 luGlyLysTrpCysIleAsnGlyLys-CysValAsnLysAsnHisArgLysHisPheAsp 555
Db      1818 CTGGGCACCTCTGCTCAGAAGGCAAGCTGTCTACCTGAGGAGGAAGTGGAGAGGCCCAAG 1759

Qy       556 ThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCys 575
Db      1758 CCCGTGGTAGATGGAGGCTGGGCACCGTGGGGACCCTGGGGAGAATGTTCTCGGACCTGT 1699

Qy       576 GlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGly 595
Db      1698 GGAGGAGGAGTACAGTTTTCACACCGTGAGTGCAAGGACCCCGAGCCTCAGAATGGAGGA 1639

Qy       596 LysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAsp 615
Db      1638 AGATACTGCCTGGGTCGGAGAGCCAAGTACCAGTCATGCCACACGGAGGAATGCCCCCCT 1579

Qy       616 AsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAla 635
Db      1578 ---GACGGGAAAAGCTTCAGGGAGCAGCAGTGTGAGAAGTATAATGCCTACAATTACACT 1522

Qy       636 SerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLys 655
Db      1521 GACATG---GACGGGAATCTCCTGCAGTGGGTCCCCAAGTATGCTGGGGTGTCCCCCCGG 1465
```



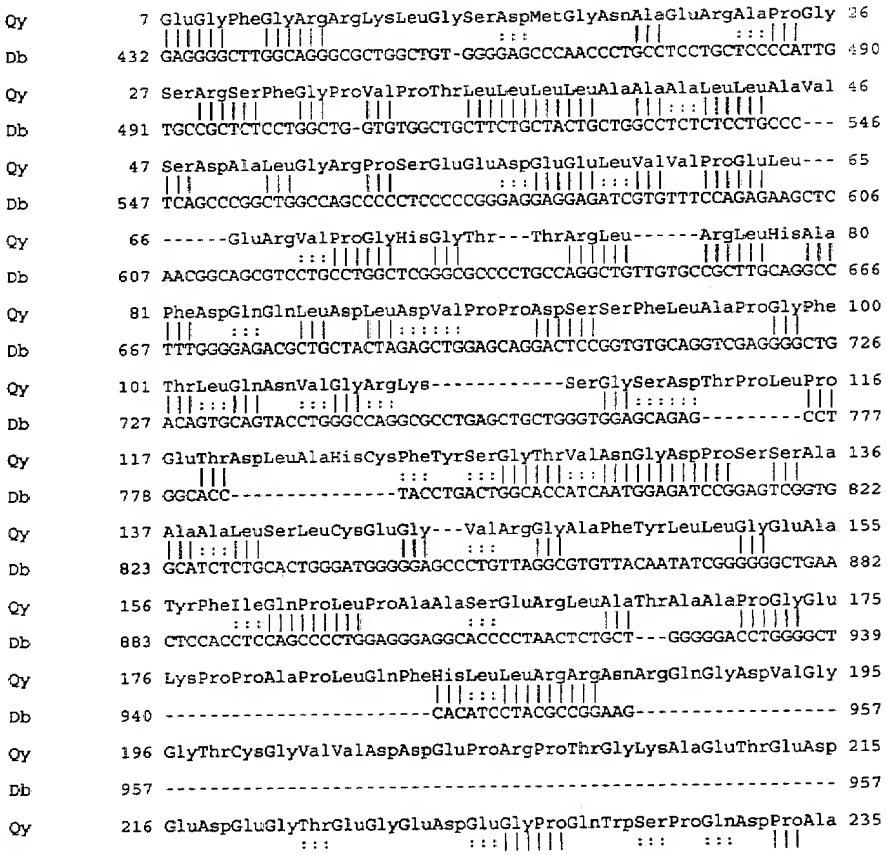
RESULT 9
US-09-122-126B-1
; Sequence 1, Application US/09122126B
; Patent No. 6451575

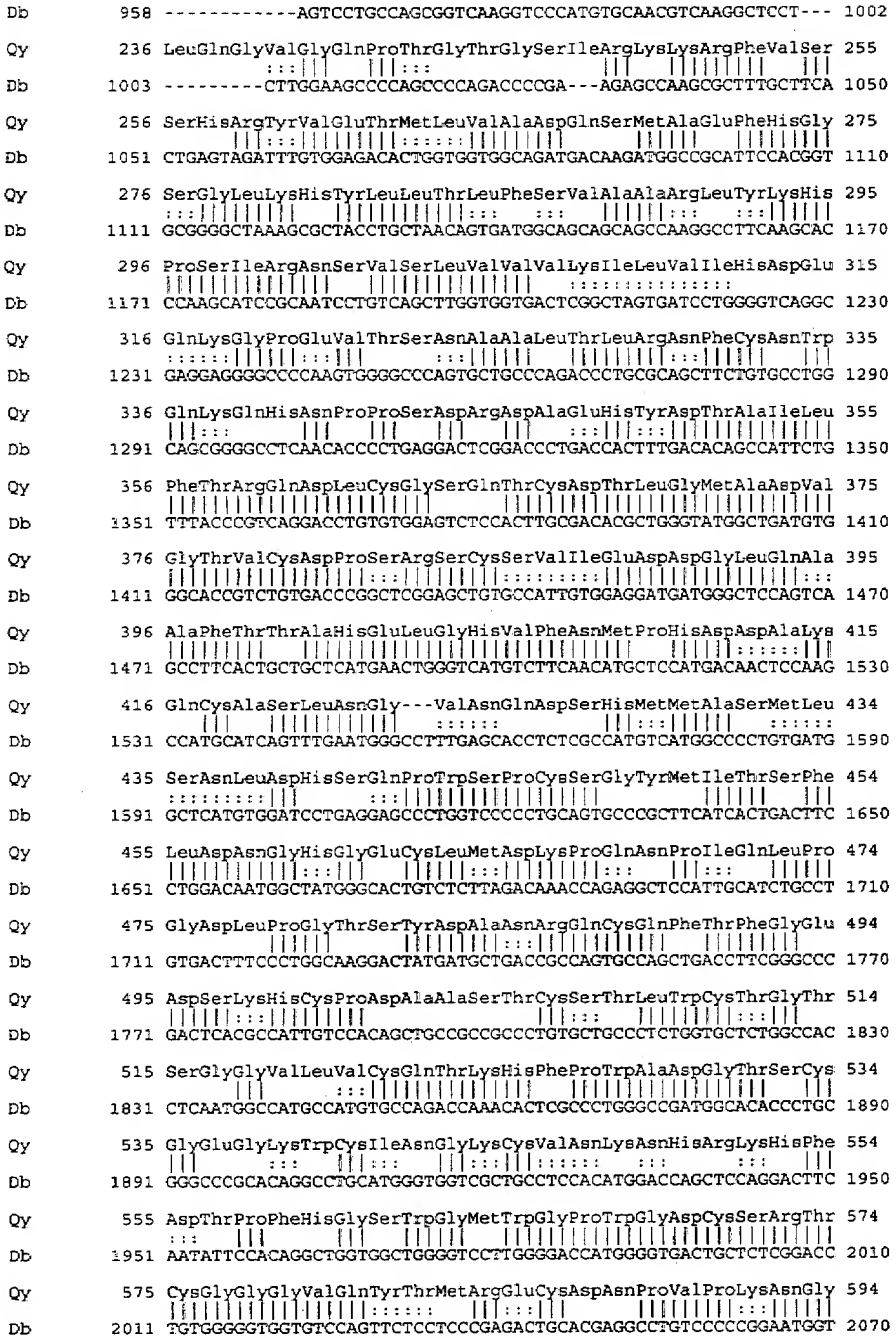
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-122-126B-1

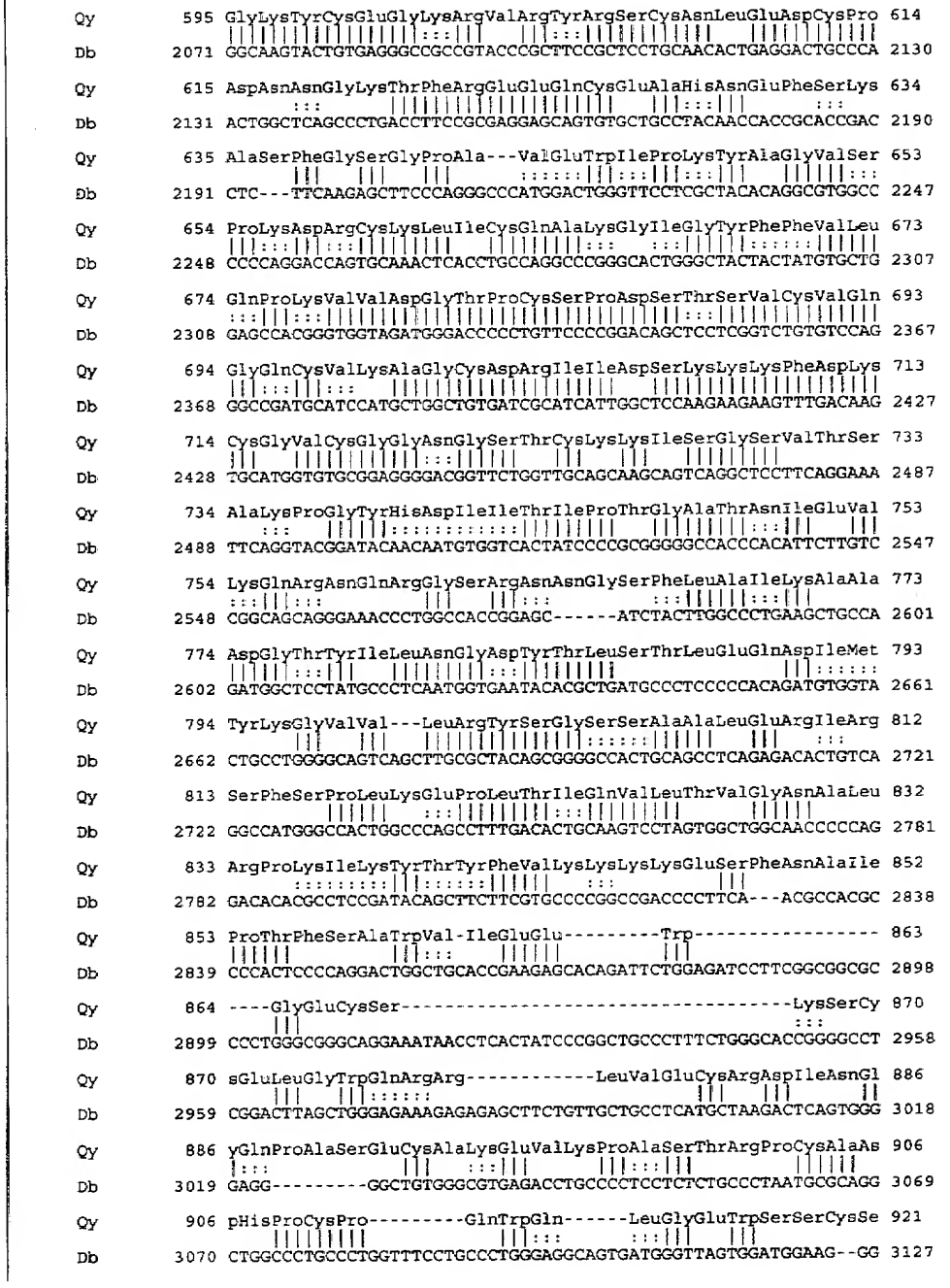
Alignment Scores:

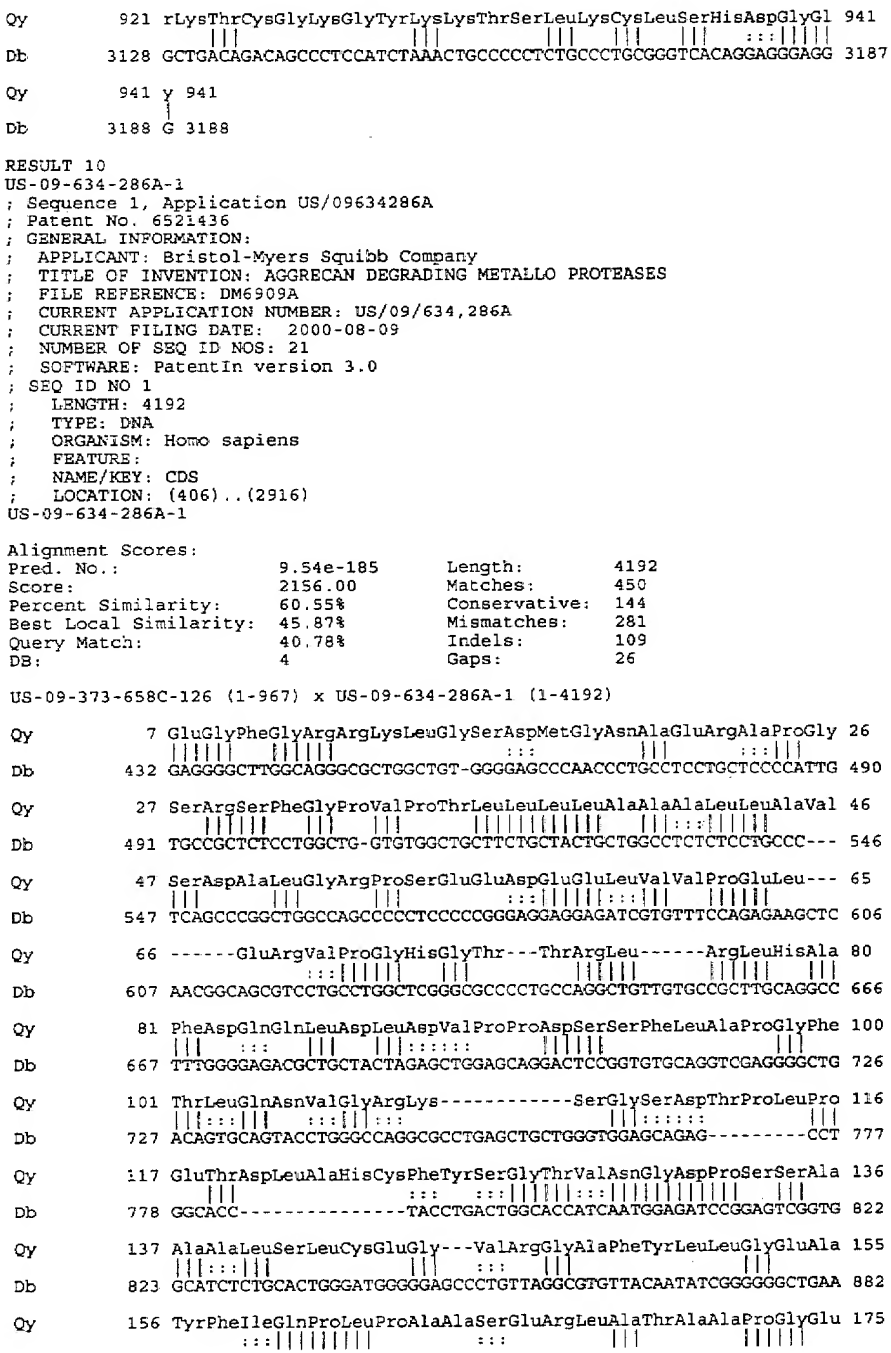
Pred. No.:	9.54e-185	Length:	4192
Score:	2156.00	Matches:	450
Percent Similarity:	60.55%	Conservative:	144
Best Local Similarity:	45.87%	Mismatches:	281
Query Match:	40.78%	Indels:	109
DB:	4	Gaps:	26

US-09-373-658C-126 (1-967) x US-09-122-126B-1 (1-4192)









```
Qy        921 rLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGl 941
Db       3128 GCTGACAGACAGCCCTCCATCTAAACTGCCCCCTCTGCCCTGCGGGTCACAGGAGGGAGG 3187

Qy        941 y 941
Db       3188 G 3188
```

RESULT 10
US-09-634-286A-1
; Sequence 1, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-634-286A-1

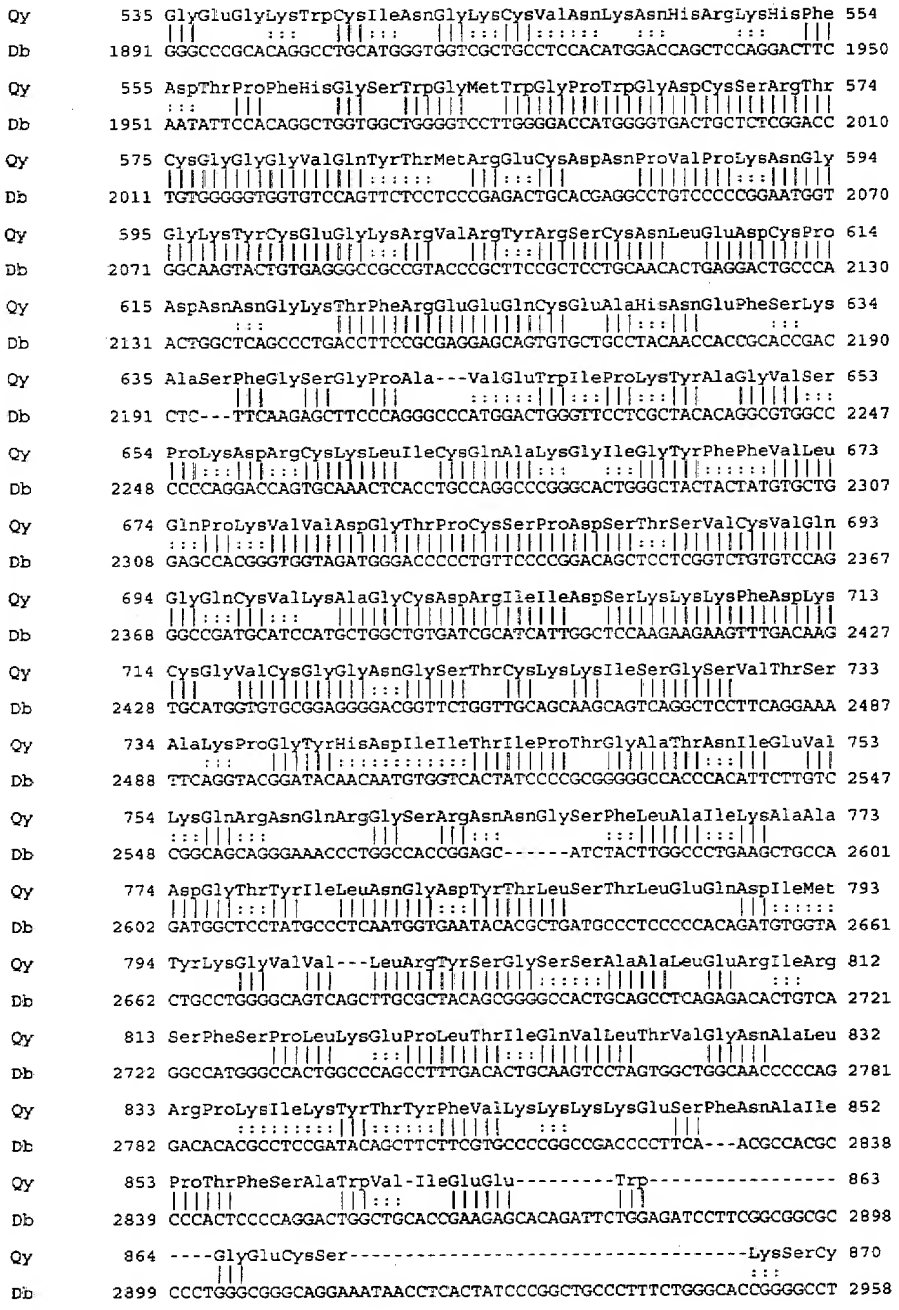
Alignment Scores:

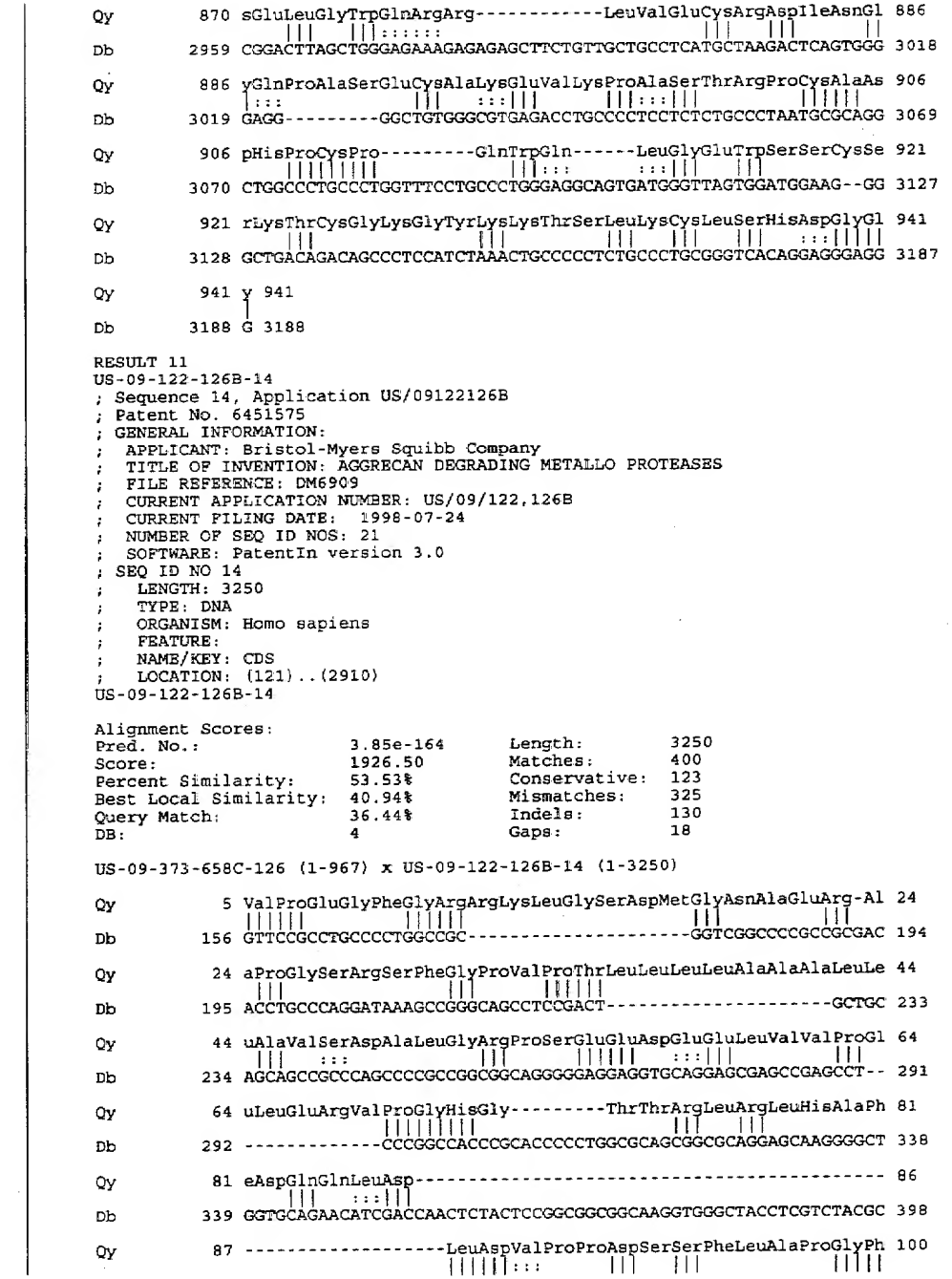
Pred. No.:	9.54e-185	Length:	4192
Score:	2156.00	Matches:	450
Percent Similarity:	60.55%	Conservative:	144
Best Local Similarity:	45.87%	Mismatches:	281
Query Match:	40.78%	Indels:	109
DB:	4	Gaps:	26

US-09-373-658C-126 (1-967) x US-09-634-286A-1 (1-4192)

```
Qy          7 GluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluArgAlaProGly 26
Db        432 GAGGGGCTTGGCAGGGCGCTGGCTGT-GGGGAGCCCAACCCTGCCTCCTGCTCCCCATTG 490

Qy         27 SerArgSerPheGlyProValProThrLeuLeuLeuLeuAlaAlaAlaLeuLeuAlaVal 46
Db        491 TGCCGCTCTCCTGGCTG-GTGTGGCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCC--- 546

Qy         47 SerAspAlaLeuGlyArgProSerGluGluAspGluGluLeuValValProGluLeu--- 65
Db        547 TCAGCCCGGCTGGCCAGCCCCCTCCCCCGGGAGGAGGAGATCGTGTTTCCAGAGAAGCTC 606

Qy         66 ------GluArgValProGlyHisGlyThr---ThrArgLeu------ArgLeuHisAla 80
Db        607 AACGGCAGCGTCCTGCCTGGCTCGGGCGCCCCTGCCAGGCTGTTGTGCCGCTTGCAGGCC 666

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db        667 TTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTG 726

Qy        101 ThrLeuGlnAsnValGlyArgLys-----------SerGlySerAspThrProLeuPro 116
Db        727 ACAGTGCAGTACCTGGGCCAGGCGCCTGAGCTGCTGGGTGGAGCAGAG---------CCT 777

Qy        117 GluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAla 136
Db        778 GGCACC--------------TACCTGACTGGCACCATCAATGGAGATCCGGAGTCGGTG 822

Qy        137 AlaAlaLeuSerLeuCysGluGly---ValArgGlyAlaPheTyrLeuLeuGlyGluAla 155
Db        823 GCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAA 882

Qy        156 TyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlu 175
```

```
Db        883 CTCCACCTCCAGCCCCTGGAGGGAGGCACCCCTAACTCTGCT---GGGGGACCTGGGGCT 939

Qy        176 LysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGly 195
Db        940 ----------------------CACATCCTACGCCGGAAG---------------- 957

Qy        196 GlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAsp 215
Db        957 ------------------------------------------------------------ 957

Qy        216 GluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAla 235
Db        958 -----------AGTCCTGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCT--- 1002

Qy        236 LeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSer 255
Db       1003 ---------CTTGGAAGCCCCAGCCCCAGACCCCGA---AGAGCCAAGCGCTTTGCTTCA 1050

Qy        256 SerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGly 275
Db       1051 CTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGT 1110

Qy        276 SerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHis 295
Db       1111 GCGGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCTTCAAGCAC 1170

Qy        296 ProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGlu 315
Db       1171 CCAAGCATCCGCAATCCTGTCAGCTTGGTGGTGACTCGGCTAGTGATCCTGGGGTCAGGC 1230

Qy        316 GlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrp 335
Db       1231 GAGGAGGGGCCCCAAGTGGGGCCCAGTGCTGCCCAGACCCTGCGCAGCTTCTGTGCCTGG 1290

Qy        336 GlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeu 355
Db       1291 CAGCGGGGCCTCAACACCCCTGAGGACTCGGACCCTGACCACTTTGACACAGCCATTCTG 1350

Qy        356 PheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspVal 375
Db       1351 TTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCGACACGCTGGGTATGGCTGATGTG 1410

Qy        376 GlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAla 395
Db       1411 GGCACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCA 1470

Qy        396 AlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLys 415
Db       1471 GCCTTCACTGCTGCTCATGAACTGGGTCATGTCTTCAACATGCTCCATGACAACTCCAAG 1530

Qy        416 GlnCysAlaSerLeuAsnGly---ValAsnGlnAspSerHisMetMetAlaSerMetLeu 434
Db       1531 CCATGCATCAGTTTGAATGGGCCTTTGAGCACCTCTCGCCATGTCATGGCCCCTGTGATG 1590

Qy        435 SerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPhe 454
Db       1591 GCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCCGCTTCATCACTGACTTC 1650

Qy        455 LeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuPro 474
Db       1651 CTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCT 1710

Qy        475 GlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGlu 494
Db       1711 GTGACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCC 1770

Qy        495 AspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThr 514
Db       1771 GACTCACGCCATTGTCCACAGCTGCCGCCGCCCTGTGCTGCCCTCTGGTGCTCTGGCCAC 1830

Qy        515 SerGlyGlyValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSerCys 534
Db       1831 CTCAATGGCCATGCCATGTGCCAGACCAAACACTCGCCCTGGGCCGATGGCACACCCTGC 1890
```



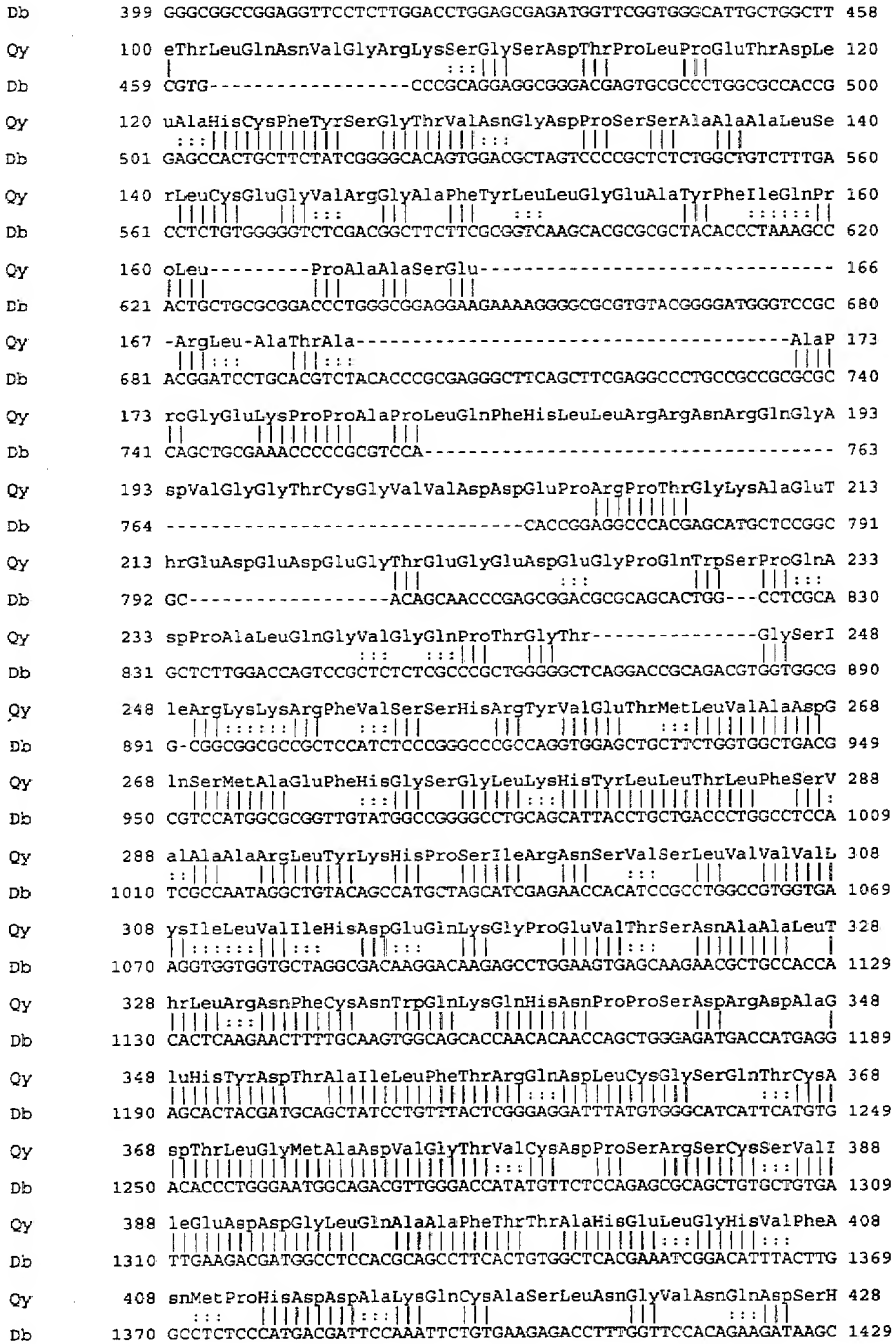


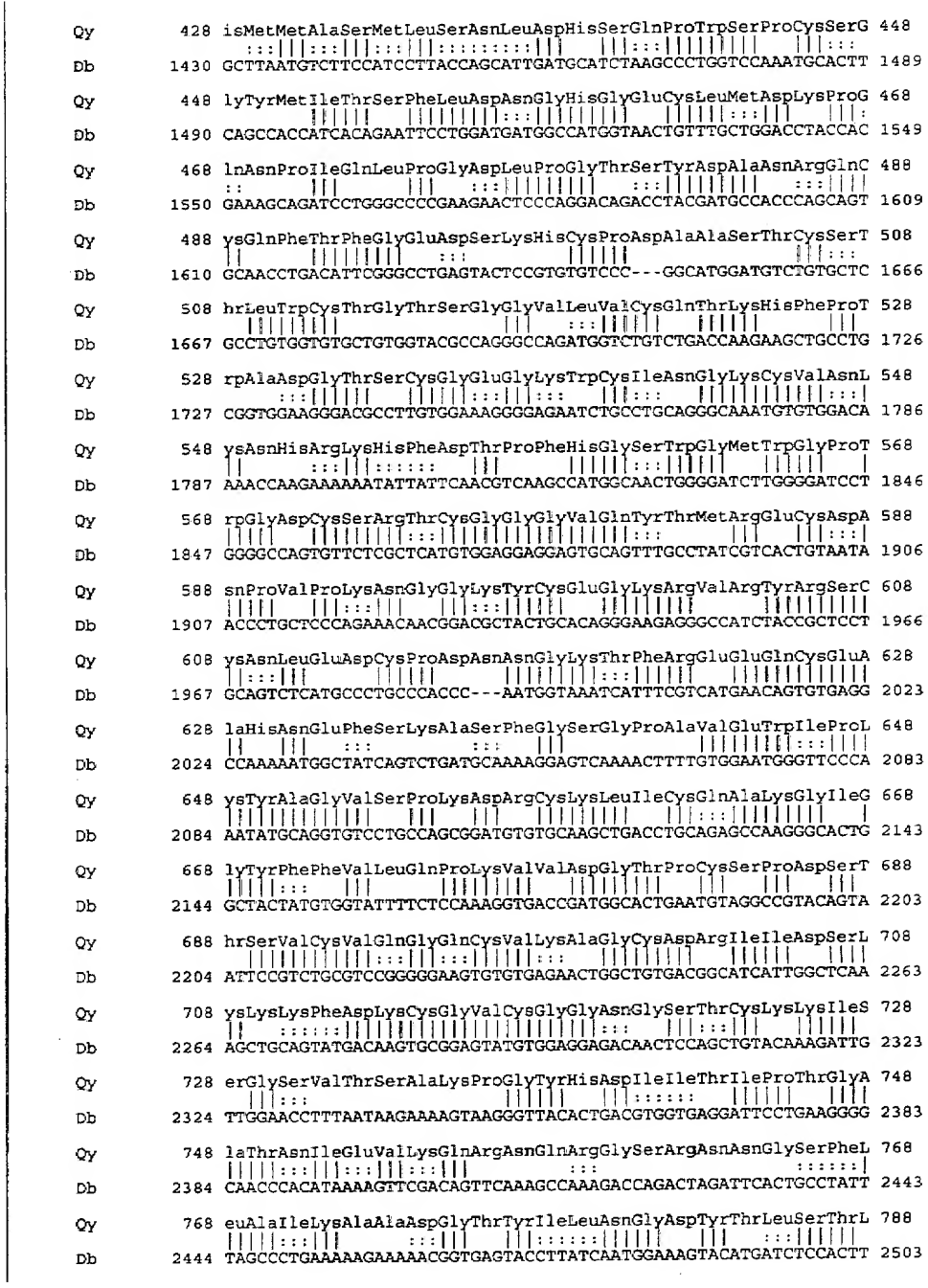
RESULT 11
US-09-122-126B-14
; Sequence 14, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-122-126B-14

Alignment Scores:

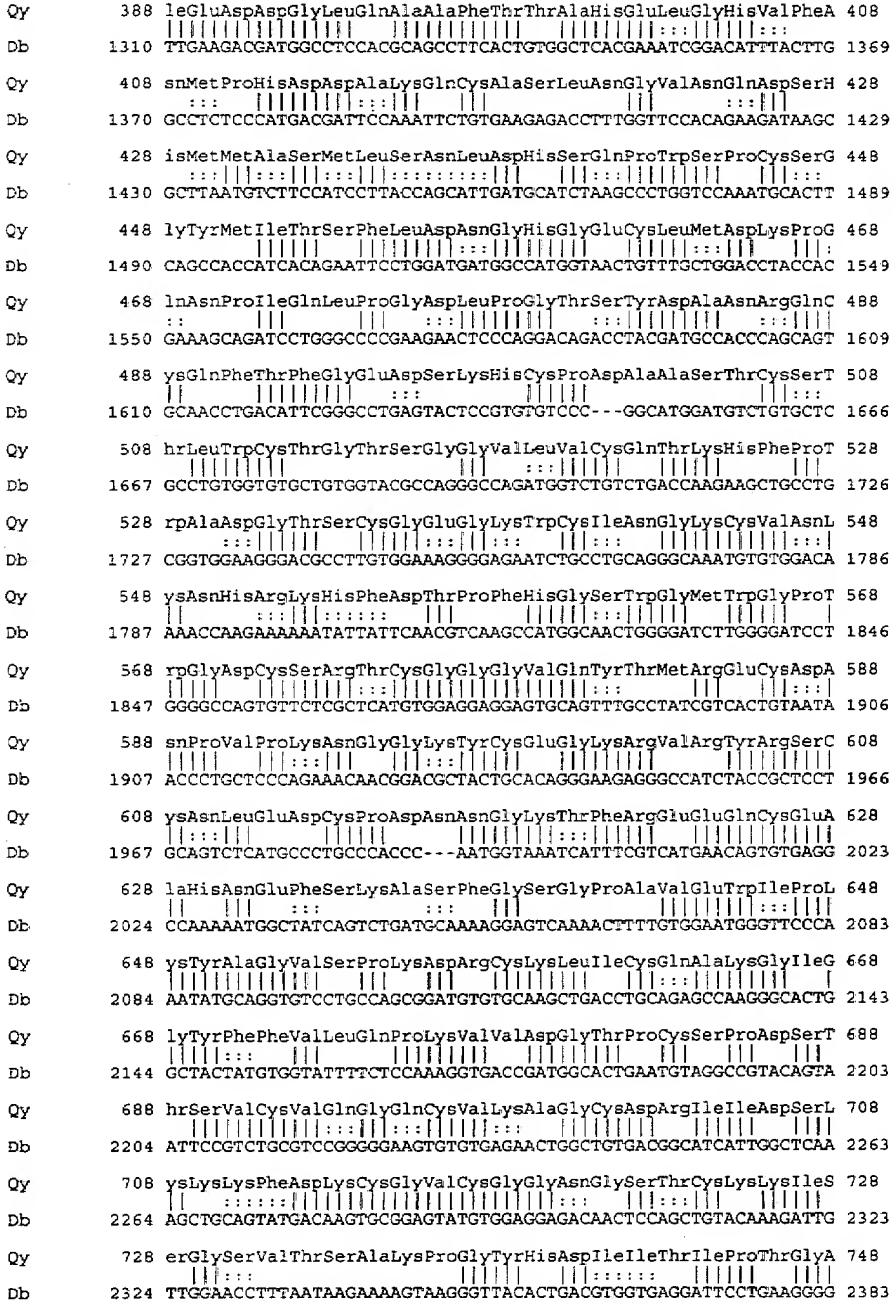
Pred. No.:	3.85e-164	Length:	3250
Score:	1926.50	Matches:	400
Percent Similarity:	53.53%	Conservative:	123
Best Local Similarity:	40.94%	Mismatches:	325
Query Match:	36.44%	Indels:	130
DB:	4	Gaps:	18

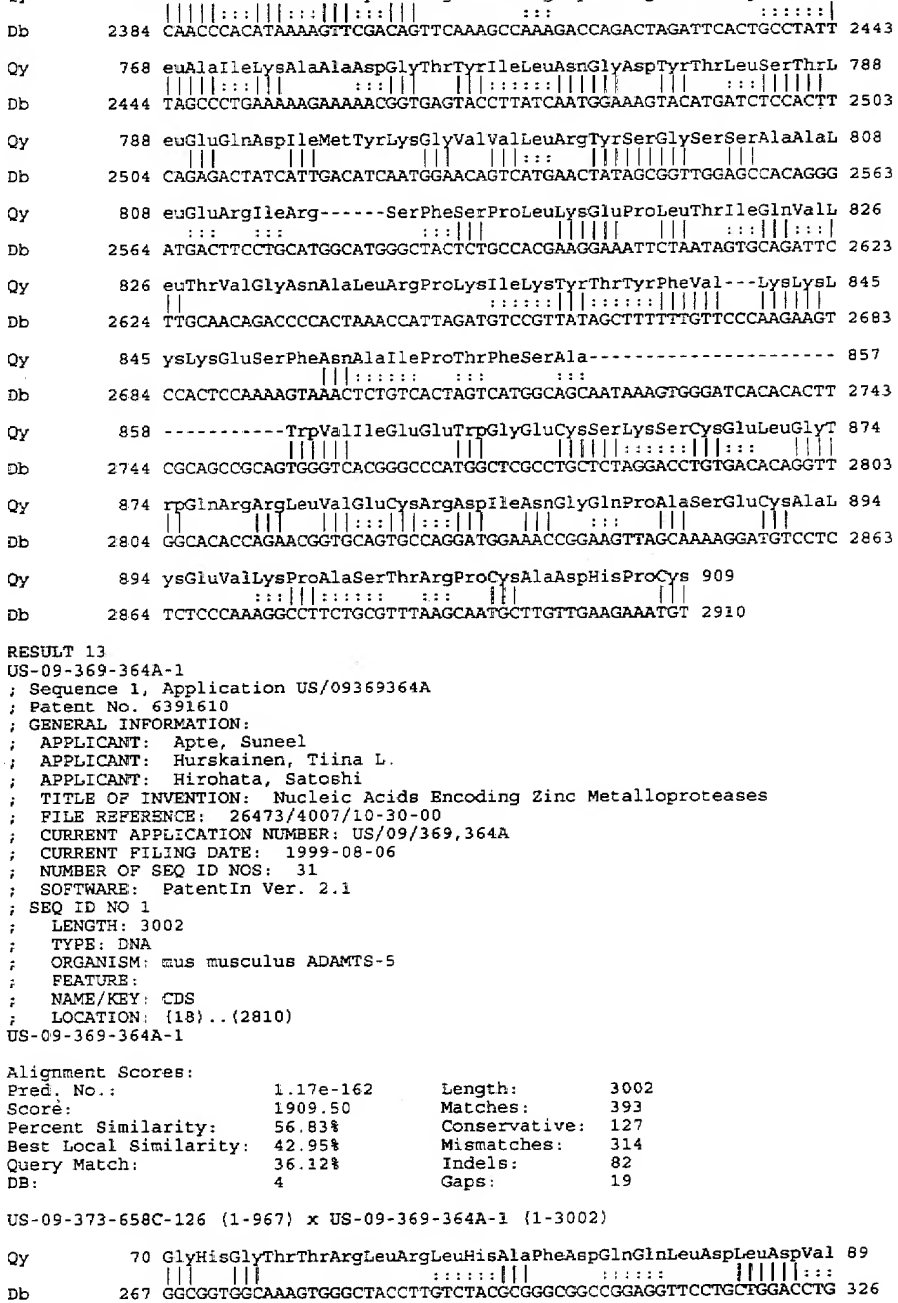
US-09-373-658C-126 (1-967) x US-09-122-126B-14 (1-3250)





```
Qy        788 euGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaL 808
Db       2504 CAGAGACTATCATTGACATCAATGGAACAGTCATGAACTATAGCGGTTGGAGCCACAGGG 2563

Qy        808 euGluArgIleArg------SerPheSerProLeuLysGluProLeuThrIleGlnValL 826
Db       2564 ATGACTTCCTGCATGGCATGGGCTACTCTGCCACGAAGGAAATTCTAATAGTGCAGATTC 2623

Qy        826 euThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheVal---LysLysL 845
Db       2624 TTGCAACAGACCCCACTAAACCATTAGATGTCCGTTATAGCTTTTTTGTTCCCAAGAAGT 2683

Qy        845 ysLysGluSerPheAsnAlaIleProThrPheSerAla---------------------- 857
Db       2684 CCACTCCAAAAGTAAACTCTGTCACTAGTCATGGCAGCAATAAAGTGGGATCACACACTT 2743

Qy        858 -----------TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyT 874
Db       2744 CGCAGCCGCAGTGGGTCACGGGCCCATGGCTCGCCTGCTCTAGGACCTGTGACACAGGTT 2803

Qy        874 rpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaL 894
Db       2804 GGCACACCAGAACGGTGCAGTGCCAGGATGGAAACCGGAAGTTAGCAAAAGGATGTCCTC 2863

Qy        894 ysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 909
Db       2864 TCTCCCAAAGGCCTTCTGCGTTTAAGCAATGCTTGTTGAAGAAATGT 2910

RESULT 12
US-09-634-286A-14
; Sequence 14, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
;  FILE REFERENCE: DM6909A
;  CURRENT APPLICATION NUMBER: US/09/634,286A
;  CURRENT FILING DATE:  2000-08-09
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 3250
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (121)..(2910)
US-09-634-286A-14

Alignment Scores:
Pred. No.:              3.85e-164      Length:          3250
Score:                  1926.50        Matches:         400
Percent Similarity:     53.53%         Conservative:    123
Best Local Similarity:  40.94%         Mismatches:      325
Query Match:            36.44%         Indels:          130
DB:                     4              Gaps:            18

US-09-373-658C-126 (1-967) x US-09-634-286A-14 (1-3250)

Qy          5 ValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluArg-Al 24
Db        156 GTTCCGCCTGCCCCTGGCCGC--------------------GGTCGGCCCCGCCGCGAC 194

Qy         24 aProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAlaAlaAlaLeuLe 44
Db        195 ACCTGCCCAGGATAAAGCCGGGCAGCCTCCGACT--------------------GCTGC 233

Qy         44 uAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeuValValProGl 64
Db        234 AGCAGCCGCCCAGCCCCGCCGGCGGCAGGGGGAGGAGGTGCAGGAGCGAGCCGAGCCT-- 291

Qy         64 uLeuGluArgValProGlyHisGly---------ThrThrArgLeuArgLeuHisAlaPh 81
Db        292 ------------CCCGGCCACCCGCACCCCCTGGCGCAGCGGCGCAGGAGCAAGGGGCT 338

Qy         81 eAspGlnGlnLeuAsp---------------------------------------------- 86
Db        339 GGTGCAGAACATCGACCAACTCTACTCCGGCGGCGGCAAGGTGGGCTACCTCGTCTACGC 398

Qy         87 ------------------LeuAspValProProAspSerSerPheLeuAlaProGlyPh 100
Db        399 GGGCGGCCGGAGGTTCCTCTTGGACCTGGAGCGAGATGGTTCGGTGGGCATTGCTGGCTT 458

Qy        100 eThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLe 120
Db        459 CGTG------------------CCCGCAGGAGGCGGGACGAGTGCGCCCTGGCGCCACCG 500

Qy        120 uAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSe 140
Db        501 GAGCCACTGCTTCTATCGGGGCACAGTGGACGCTAGTCCCCGCTCTCTGGCTGTCTTTGA 560

Qy        140 rLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPr 160
Db        561 CCTCTGTGGGGGTCTCGACGGCTTCTTCGCGGTCAAGCACGCGCGCTACACCCTAAAGCC 620

Qy        160 oLeu---------ProAlaAlaSerGlu---------------------------------- 166
Db        621 ACTGCTGCGCGGACCCTGGGCGGAGGAAGAAAAGGGGCGCGTGTACGGGGATGGGTCCGC 680

Qy        167 -ArgLeu-AlaThrAla-------------------------------------AlaP 173
Db        681 ACGGATCCTGCACGTCTACACCCGCGAGGGCTTCAGCTTCGAGGCCCTGCCGCCGCGCGC 740

Qy        173 roGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyA 193
Db        741 CAGCTGCGAAACCCCCGCGTCCA---------------------------------- 763

Qy        193 spValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluT 213
Db        764 --------------------------------CACCGGAGGCCCACGAGCATGCTCCGGC 791

Qy        213 hrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnA 233
Db        792 GC------------------ACAGCAACCCGAGCGGACGCGCAGCACTGG---CCTCGCA 830

Qy        233 spProAlaLeuGlnGlyValGlyGlnProThrGlyThr---------------GlySerI 248
Db        831 GCTCTTGGACCAGTCCGCTCTCTCGCCCGCTGGGGGCTCAGGACCGCAGACGTGGTGGCG 890

Qy        248 leArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspG 268
Db        891 G-CGGCGGCGCCGCTCCATCTCCCGGGCCCGCCAGGTGGAGCTGCTTCTGGTGGCTGACG 949

Qy        268 lnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerV 288
Db        950 CGTCCATGGCGCGGTTGTATGGCCGGGGCCTGCAGCATTACCTGCTGACCCTGGCCTCCA 1009

Qy        288 alAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValValL 308
Db       1010 TCGCCAATAGGCTGTACAGCCATGCTAGCATCGAGAACCACATCCGCCTGGCCGTGGTGA 1069

Qy        308 ysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuT 328
Db       1070 AGGTGGTGGTGCTAGGCGACAAGGACAAGAGCCTGGAAGTGAGCAAGAACGCTGCCACCA 1129

Qy        328 hrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaG 348
Db       1130 CACTCAAGAACTTTGCAAGTGGCAGCACCAACACAACCAGCTGGGAGATGACCATGAGG 1189

Qy        348 luHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysA 368
Db       1190 AGCACTACGATGCAGCTATCCTGTTTACTCGGGAGGATTTATGTGGGCATCATTCATGTG 1249

Qy        368 spThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValI 388
Db       1250 ACACCCTGGGAATGGCAGACGTTGGGACCATATGTTCTCCAGAGCGCAGCTGTGCTGTGA 1309
```



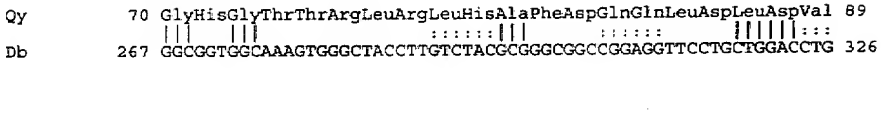


RESULT 13
US-09-369-364A-1
; Sequence 1, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3002
; TYPE: DNA
; ORGANISM: mus musculus ADAMTS-5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(2810)
US-09-369-364A-1

Alignment Scores:

Pred. No.:	1.17e-162	Length:	3002
Score:	1909.50	Matches:	393
Percent Similarity:	56.83%	Conservative:	127
Best Local Similarity:	42.95%	Mismatches:	314
Query Match:	36.12%	Indels:	82
DB:	4	Gaps:	19

US-09-373-658C-126 (1-967) x US-09-369-364A-1 (1-3002)



```
Db       2400 TCAGAGACCATCATCGACATCAATGGTACCGTCATGAACTACAGTGGATGGAGCCACAGA 2459

Qy        808 LeuGluArgIleArg------SerPheSerProLeuLysGluProLeuThrIleGlnVal 825

Db       2460 GATGATTTTTTACATGGGATGGGCTATTCAGCCACAAAAGAAATCCTGATCGTGCAGATC 2519

Qy        826 LeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheVal---LysLys 844

Db       2520 CTTGCCACAGACCCAACTAAAGCGCTAGGCGTCCGTTACAGCTTTTTTGTTCCCAAGAAG 2579

Qy        845 LysLysGluSerPheAsnAlaIle--------------------------------Pro 853

Db       2580 ACCACTCAAAAAGTAAACTCTGTCATCAGCCATGGCAGCAACAAGGTGGGACCACACTCT 2639

Qy        854 ThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGly 873

Db       2640 ACACAGCTGCAGTGGGTGACAGGTCCATGGCTGGCCTGCTCCAGGACCTGTGACACAGGC 2699

Qy        874 TrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893

Db       2700 TGGCACACTAGGACCGTGCAGTGCCAGGATGGAAACAGGAAATTAGCTAAAGGATGCCTT 2759

Qy        894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCys---ProGlnTrp 912

Db       2760 CTCTCTCAGAGGCCTTCTGCATTTAAGCAATGTCTGCTGAAGAAATGTTAGCCTGTG--- 2816

Qy        913 GlnLeuGlyGluTrpSerSerCysSerLys--------------------------Thr 923

Db       2817 ---------GTTTACTCTAA-TGCACAAAAAAACAACAGGAGGATCATCGCAGATACAGC 2866

Qy        924 CysGly------LysGlyTyrLysLysThrSerLeuLysCysLeu 936

Db       2867 TGTGGTGAAGACAAGGCCTACCCAAAGCACAGAAAGTCATGCCTT 2911
```

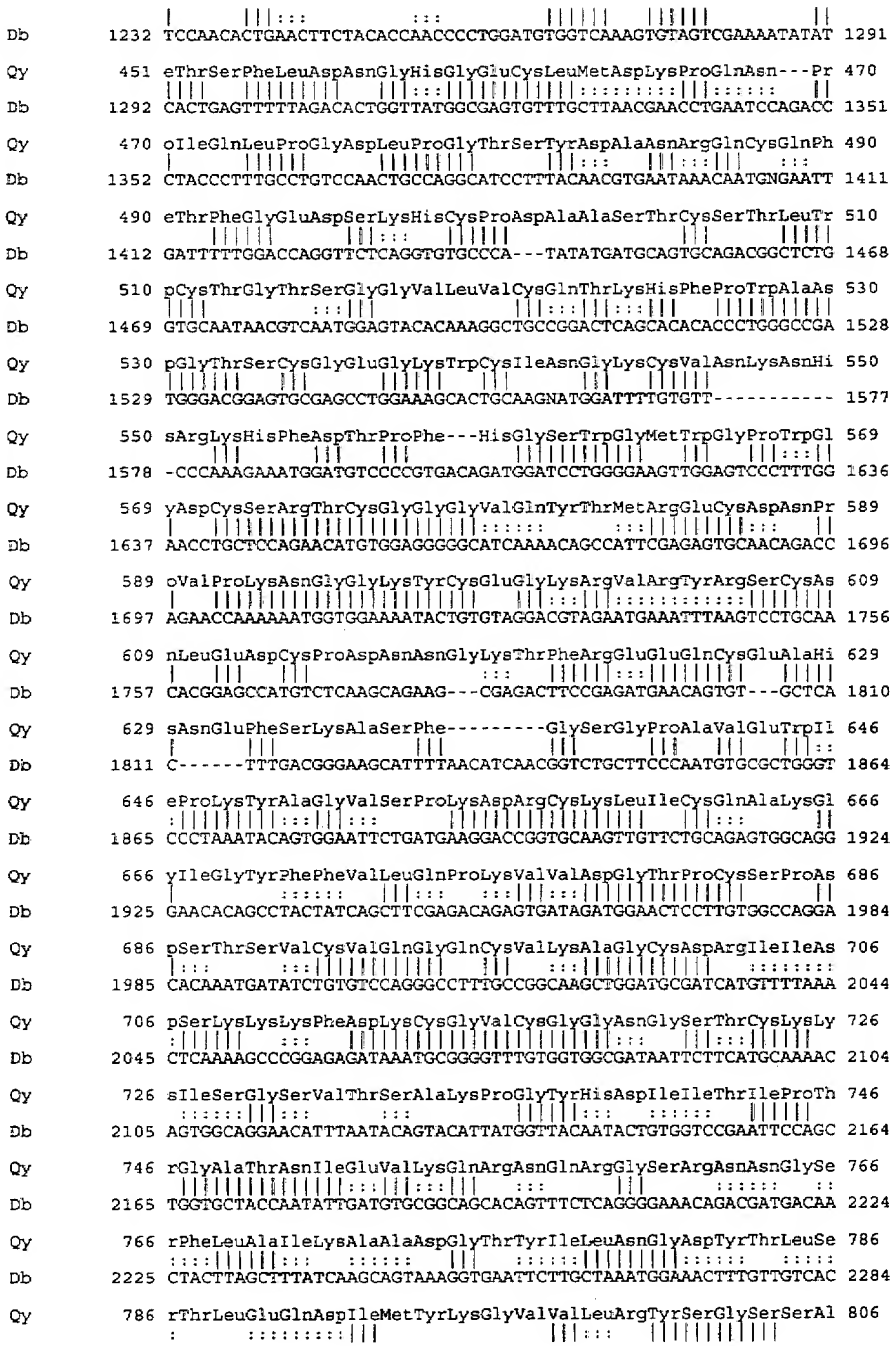
RESULT 14
US-09-369-364A-12
; Sequence 12, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5804
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(5648)
; NAME/KEY: misc_feature
; LOCATION: (1406)
; OTHER INFORMATION: n=T
; NAME/KEY: misc_feature
; LOCATION: (1563)
; OTHER INFORMATION: n=T
US-09-369-364A-12

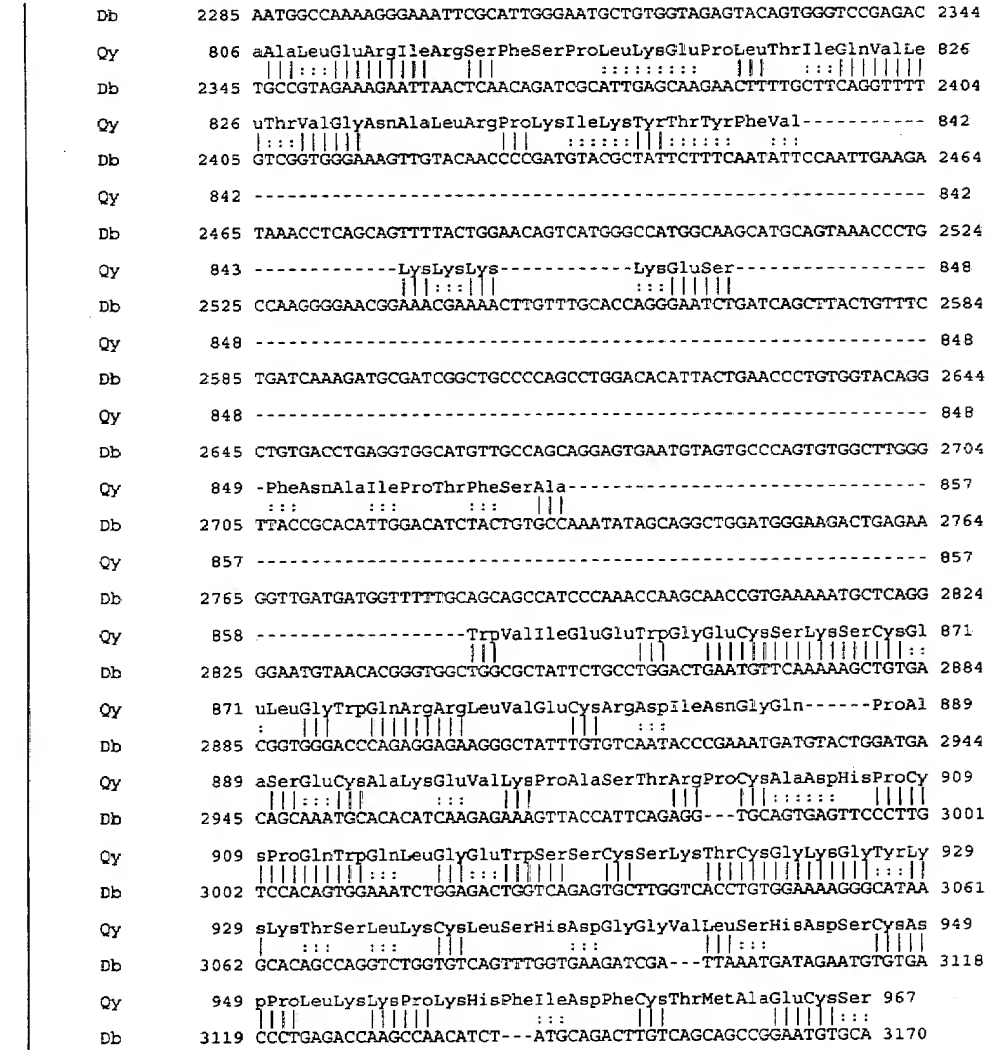
Alignment Scores:

Pred. No.:	7e-148	Length:	5804
Score:	1751.50	Matches:	367
Percent Similarity:	51.03%	Conservative:	153
Best Local Similarity:	36.02%	Mismatches:	307
Query Match:	33.13%	Indels:	193
DB:	4	Gaps:	24

US-09-373-658C-126 (1-967) x US-09-369-364A-12 (1-5804)

```
Qy         77 ArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeu 96

Db        309 CGCCTCTCTGCCTTCGGCCAGCAGTTTCTATTTAATCTCACCGCCAATGCCGGATTTATC 368

Qy         97 AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu--- 115

Db        369 GCTCCACTGTTCACTGTCACCCTCCTTGGGACGCCCGGGGTGAATCAGACCAAGTTTTAT 428

Qy        116 ------ProGluThrAspLeuAlaHisCysPheTyr-SerGlyThrValAsnGlyAspPr 133

Db        429 TCCGAAGAGGAAGCGGAACTAAAGCACTGTTTCTACAAAAGGCTATGTCAATACCAACTC 488

Qy        133 oSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGl 153

Db        489 CGAGCACACGGCCGTCATCAGCCTCTGCTCAGGAATG---------------------- 525

Qy        153 yGluAlaTyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaPr 173

Db        526 --------------------------------AACACAAAAATAGGCACAGTAAAGAC 551

Qy        173 oGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAs 193

Db        552 AAGAAGAAAACCAGA-GCAAGAAAATGGGGAGAA------AGGATTAACCTGGCTGGTGA 604

Qy        193 pValGlyGly---ThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGl 212

Db        605 CGTAGCAGCATTAAACAGCGGCTTAGCAACAGAGGCATTTTCTGCTTATGGTAATAAGAC 664

Qy        212 uThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGl 232

Db        665 GGACAACACAAGAGAAAAGAGGACCCACAGA---------------------------- 695

Qy        232 nAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysAr 252

Db        696 ------------------------------------------------AGGACAAAACG 706

Qy        252 gPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGl 272

Db        707 TTTTTTATCCTATCCACGGTTTGTAGAAGTCTTGGTGGTGGCAGACAACAGAATGGTTTC 766

Qy        272 uPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLe 292

Db        767 ATACCATGGAGAAAACCTTCAACACTATATTTAACTTTAATGTCAATTGTAGCCTCTAT 826

Qy        292 uTyrLysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIl 312

Db        827 CTATAAAGACCCAAGTATTGGAAATTTAATTAATATTGTTATTGTGAACTTAATTGTGAT 886

Qy        312 eHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPh 332

Db        887 TCATAATGAACAGGATGGGCCTTCCATATCTTTTAATGCTCAGACAACATTAAAAAACTT 946

Qy        332 eCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspTh 352

Db        947 TTGCCAGTGGCAGCATTCGAACAGTCCA-----------GGTGGAATCCATCATGATAC 994

Qy        352 rAlaIleLeuPheThrArgGlnAspLeuCys---GlySerGlnThrCysAspThrLeuGl 371

Db        995 TGCTGTTCTCTTAACAAGACAGGATATCTGCAGAGCTCACGACAAATGTGATACCTTAGG 1054

Qy        371 yMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAs 391

Db       1055 CCTGGCTGAACTGGGAACCATTTGTGATCCCTATAGAAGCTGTTCTATTAGTGAAGATAG 1114

Qy        391 pGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHi 411

Db       1115 TGGATTGAGTACAGCTTTTACGATCGCCCATGAGCTGGGCCATGTGTTTAACATGCCTCA 1174

Qy        411 sAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAl 431

Db       1175 TGATGACAACAACAAATGTAAAGAA---GAAGGAGTTAAGAGTCCCCAGCATGTCATGGC 1231

Qy        431 aSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIl 451
```





RESULT 15
US-09-369-364A-14
; Sequence 14, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Mus musculus ADAMTS-9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2623)
US-09-369-364A-14

Alignment Scores:

Pred. No.:	6.73e-136	Length:	2625
Score:	1613.00	Matches:	341
Percent Similarity:	55.99%	Conservative:	145
Best Local Similarity:	39.29%	Mismatches:	312
Query Match:	30.51%	Indels:	71
DB:	4	Gaps:	26

US-09-373-658C-126 (1-967) x US-09-369-364A-14 (1-2625)

```
Qy        137 AlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyr 156
Db          8 GCGGTCATCAGCCTGTGCTCCGGAATGATGGGCACGTTCCGCTCTCACGATGGAGATTAT 67

Qy        157 PheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLys 176
Db         68 TTCATTGAACCACTGCAGTCTGTGGATGAGCAA-----------GAGGATGAAGAGGAA 115

Qy        177 ProProAlaProLeuGlnPheHisLeuLeuArgArgAsn----------ArgGlnGly 192
Db        116 CAAAACAAACCC---------CACATTATTTATAGGCACAGCACCCCTCAGAGGGAACCC 166

Qy        193 AspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGlu 212
Db        167 TCCACAGGAAAGCATGCCTGTGCCACCTCAGAACTCAAAAATAGTCACAGTAAAGA-CAA 225

Qy        213 ThrGluAspGluAspGluGlyThrGluGlyGluAsp---------------------- 224
Db        226 GCGGAAAATCAGAATGCGAAAACGGAGAAAGAGGAATAGCCTGGCTGACGACGTGGCACT 285

Qy        225 --------------------GluGlyProGlnTrpSerProGlnAspProAlaLeuGln 237
Db        286 GCTAAAGAGCGGTTTGGCAACAAAGGTGCTCTCTGGCTATAGCAA---CCAGACAAACAA 342

Qy        238 GlyValGlyGlnProThrGlyThr-GlySerIleArgLysLysArgPheValSerSerHi 257
Db        343 CACAAGGGACAG---------ATGGAACCACAAAAGAACCAAACGCTTTCTGTCCTACCC 393

Qy        257 sArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGl 277
Db        394 ACGGTTTGTAGAGGTGATGGTGGTGGCTGACCACAGGATGGTTTTATACCACGGAGCAAA 453

Qy        277 yLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSe 297
Db        454 CCTTCAACATTATATCTTAACCTTAATGTCCATTGTAGCTTCTATCTATAAAGACTCAAG 513

Qy        297 rIleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLy 317
Db        514 TATTGGAAATTTAATTAATATTGTTATTGTGAACTTAGTTGTGATTCATAATGAACAGGA 573

Qy        317 sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLy 337
Db        574 AGGACCTTACATAAATTTCAATGCCCAGACAACATTAAAGAACTTTTGCCAGTGGCAGCA 633

Qy        337 sGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheTh 357
Db        634 CTCAAAGAAC---------TACTTGGGTGGGATTCAGCACGACACAGCCGTTCTGGTCAC 684

Qy        357 rArgGlnAspLeuCysGlySerGln---ThrCysAspThrLeuGlyMetAlaAspValGl 376
Db        685 AAGGGAAGATATCTGCAGAGCTCAGGACAAATGTGACACCTTAGGTCTTGCTGAACTGGG 744

Qy        376 yThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAl 396
Db        745 AACCATTTGCGACCCCTACCGAAGCTGTTCCATTAGTGAAGACAGTGGGCTGAGCACAGC 804

Qy        396 aPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGl 416
Db        805 TTTCACAATAGCTCACGAGCTGGGCCATGTGTTTAATATGCCTCACGATGACAGCAATAA 864

Qy        416 nCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAs 436
Db        865 ATGCAAAGAA---GAAGGAGTTAAGAGTCCCCAGCATGTCATGGCACCAACACTGAACTT 921

Qy        436 nLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAs 456
Db        922 CTACACCAACCCCTGGATGTGGTCAAAGTGCAGTCGGAAATACATCACTGAGTTCCTAGA 981

Qy        456 pAsnGlyHisGlyGluCysLeuMetAspLysPro---GlnAsnProIleGlnLeuProGl 475
Db        982 CACTGGGTACGGAGAGTGCTTGCTGAATGAACCTGCATCCAGGACCTATCCTTTGCCTTC 1041

Qy        475 yAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAs 495
Db       1042 CCAACTGCCCGGCCTTCTCTACAACGTGAATAAACAATGTGAACTGATTTTTGGGCCAGG 1101

Qy        495 pSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSe 515
Db       1102 CTCTCAAGTGTGCCCC---TATATGATGCAGTGCAGACGGCTCTGGTGCAATAATGTGGA 1158

Qy        515 rGlyGlyValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGl 535
Db       1159 TGGAGCACACAAAGGCTGCAAGACTCAGCACACGCCCTGGGCAGATGGAACCGAGTGTGA 1218

Qy        535 yGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAs 555
Db       1219 GCCTGGAAAGCACTGCAAGTTTGGATTTTGTGTT-----------CCCAAAGAAATGGA 1266

Qy        555 pThrPro---PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgTh 574
Db       1267 GGGCCCTGCAATTGATGGATCCTGGGGAGGTTGGAGCCACTTTGGGACCTGCTCAAGAAC 1326

Qy        574 rCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGl 594
Db       1327 GTGTGGAGGAGGCATCAAAACAGCCATCAGAGAGTGCAACAGACCAGAGCCAAAAAATGG 1386

Qy        594 yGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysPr 614
Db       1387 TGGGAAGTACTGTGTAGGAAGGAGAATGAAGTTCAAATCCTGCAACACGGAGCCCTGCAT 1446

Qy        614 oAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLy 634
Db       1447 GAAGCAGAAG---CGAGACTTCCGAGAGGAGCAGTGT---GCTCAC------TTTGATGG 1494

Qy        634 sAlaSerPhe---------GlySerGlyProAlaValGluTrpIleProLysTyrAlaGl 651
Db       1495 CAAACACTTCAACATCAATGGTCTGCTGCCCAGCGTACGCTGGTTTCCTAAGTACAGCGG 1554

Qy        651 yValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePh 671
Db       1555 AATTTTGATGAAGGACCGGTGCAAGTTGTTCTGCAGAGTGGCAGGAAACACAGCCTACTA 1614

Qy        671 eValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCy 691
Db       1615 CCAGCTCCGAGACAGAGTGATTGACGGAACCCCTTGTGGCCAGGACACAAATGACATCTG 1674

Qy        691 sValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPh 711
Db       1675 TGTCCAAGGCCTTTGCCGGCAAGCTGGATGTGATCATATTTTAAACTCAAAGGTCCGGAA 1734

Qy        711 eAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerVa 731
Db       1735 AGATAAATGTGGGATTTGTGGTGGAGATAATTCTTCATGCAAAACAGTGGCAGGAACATT 1794

Qy        731 lThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIl 751
Db       1795 TAACACTGTCCATTATGGTTACAATACTGTTGTCCGAATTCCGGCTGGTGCTACCAGCAT 1854
```

```
Qy        751 eGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLy 771
              |:::|||:::|||   :::      |||         :::   :::::|||||||:::
Db       1855 TGACGTGCGTCAGCACAGCTTCTCAGGGAAGTCTGAGGATGACAACTACCTAGCTTTATC 1914

Qy        771 sAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAs 791
                 :::   |||   ::::::||||||||||||:::   :::|||       ::::::::
Db       1915 AAACAGTAAAGGTGAATTCCTGCTAAATGGAGACTTTGTTGTCTCCATGTCCAAAAGGGA 1974

Qy        791 pIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIl 811
              ::::             |||:::  ||||||||||||           ||||||::
Db       1975 GGTCCGCGTGGGGAGCGCCGTCATTGAGTACAGCGGATCGGACAATGTGTGTGAAAGACT 2034

Qy        811 eArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAl 831
              :          ::::::|||   |||   :::|||||||||:::||||||
Db       2035 GAACTGTACGGACCGTATCGAGGAAGAACTTCTCCTTCAGGTGTTGTCCGTGGGAAAGCT 2094

Qy        831 aLeuArgProLysIleLysTyrThrTyrPhe------ValLysLysLysGluSerPh 849
                  |||   :::::::|||::::::         ::::::   |||   :::   ||
Db       2095 GTATAACCCAGATGTGCGGTACTCATTCAATATTCCCATTGAGGACAAACCTCAGCAATT 2154

Qy        849 eAsnAlaIleProThrPheSerAlaTrpValIleGlu---GluTrpGlyGluCysSerLy 868
              |                        |||                 |||      ||||||||
Db       2155 T--------------------TACTGGAACAGTCACGGGCCGTGGCAAGCATGCAGCAA 2193

Qy        868 sSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnPr 888
              |   |||:::       :::   :::||||||      |||:::   :::
Db       2194 GCCCTGCCAAGGGGAGCGGAGACCAAAACTTGTTTGCACCAGGGAGTCTGATCAGCTAAC 2253

Qy        888 oAlaSerGlu------CysAlaLysGluValLysProAlaSer---ThrArgProCysAl 905
                 |||:::      |||   :::      :::|||        |||      |||
Db       2254 CGTTTCTGATCAAAGATGTGACCGGCTGCCCCAGCCAGGACCTGTCACTGAAGCGTGCGG 2313

Qy        905 aAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGl 925
                       :::|||   :::         |||   ||||||      |||||
Db       2314 CACAGACTGTGACTTGAGGTGGCACGTTGCCAGCAAGAGCGAATGCAGTGCCCAGTGTGG 2373

Qy        925 yLysGlyTyrLysLysThrSerLeuLysCysLeuSerHis---------AspGlyGlyVa 942
              |   ||||||:::          :::   |||       :::          |||||||
Db       2374 TTTGGGCTACCGTACTTTAGACATCCACTGTGCCAAATACAGCAGGATGGACGGGAAGAC 2433

Qy        942 lLeuSerHisAspSer------CysAspProLeuLysLysProLysHisPheIleAspPh 960
                  |||          |||             :::|||   :::      :::
Db       2434 GGAGAAGGTGGATGACAGTTTCTGTAGCAGTCAACCCAGACCGAGTAAC---CAGGAGAA 2490

Qy        960 eCysThrMetAlaGluCysSer 967
               |||:::      |||||||||
Db       2491 ATGCTCA---GGAGAGTGCAGC 2509


Search completed: June 18, 2004, 19:02:23
Job time : 292.321 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 18:42:30 ; Search time 947.831 Seconds
(without alignments)
4673.735 Million cell updates/sec

Title: US-09-373-658C-126
Perfect score: 5287
Sequence: 1 MQRAVPEGFGRRKLGSDMGN.....CDPLKKPKHFIDFCTMAECS 967

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09373658/runat_18062004_135345_10353/app_query.fasta_1.2254
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09373658_@CGN_1_1_1290_@runat_18062004_135345_10353
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5287	100.0	4014	11	US-09-989-687-125	Sequence 125, App
2	5232	99.0	4014	15	US-10-115-286-1	Sequence 1, Appli
3	5232	99.0	4676	14	US-10-105-929-1	Sequence 1, Appli
4	5224	98.8	4309	15	US-10-210-120-57	Sequence 57, Appl
5	5224	98.8	4459	16	US-10-159-563-192	Sequence 192, App
6	5224	98.8	4459	16	US-10-159-563-308	Sequence 308, App
7	5224	98.8	4760	10	US-09-971-429B-17	Sequence 17, Appl
8	5144	97.3	3261	10	US-09-373-658-1	Sequence 1, Appli
9	5144	97.3	3261	11	US-09-989-687-1	Sequence 1, Appli
10	5140.5	97.2	4848	13	US-10-425-114-26851	Sequence 26851, A
11	4287	81.1	4878	12	US-10-152-319A-1840	Sequence 1840, Ap
12	4287	81.1	4878	16	US-10-191-803-170	Sequence 170, App
13	4277.5	80.9	4180	10	US-09-373-658-20	Sequence 20, Appl
14	4277.5	80.9	4180	11	US-09-989-687-20	Sequence 20, Appl
15	3922	74.2	2184	9	US-09-445-023A-2	Sequence 2, Appli
16	3922	74.2	2184	15	US-10-097-597-2	Sequence 2, Appli
17	3922	74.2	2184	15	US-10-097-580-2	Sequence 2, Appli
18	3652	69.1	2184	9	US-09-445-023A-13	Sequence 13, Appl
19	3652	69.1	2184	15	US-10-097-597-13	Sequence 13, Appl
20	3652	69.1	2184	15	US-10-097-580-13	Sequence 13, Appl
21	3411	64.5	9248	10	US-09-373-658-21	Sequence 21, Appl
22	3411	64.5	9248	11	US-09-989-687-21	Sequence 21, Appl
23	3303	62.5	3147	9	US-09-803-589-1	Sequence 1, Appli
24	2642	50.0	3145	9	US-09-803-589-9	Sequence 9, Appli
25	2498.5	47.3	2804	16	US-10-093-463-27	Sequence 27, Appl
26	2496	47.2	3446	9	US-09-965-631-7	Sequence 7, Appli
27	2478.5	46.9	2937	13	US-10-275-107-24	Sequence 24, Appl
28	2478	46.9	2853	9	US-09-965-631-3	Sequence 3, Appli
29	2474	46.8	2867	13	US-09-741-151-1	Sequence 1, Appli
30	2461	46.5	2930	17	US-10-311-035-32	Sequence 32, Appl
31	2334	44.1	3715	13	US-10-425-114-26850	Sequence 26850, A
32	2332.5	44.1	3711	17	US-10-283-975A-398	Sequence 398, App
33	2331.5	44.1	3008	10	US-09-373-658-3	Sequence 3, Appli
34	2331.5	44.1	3008	11	US-09-989-687-3	Sequence 3, Appli
35	2271.5	43.0	3638	9	US-09-918-171A-8	Sequence 8, Appli
36	2208.5	41.8	2940	14	US-10-163-316-1	Sequence 1, Appli
37	2190.5	41.4	2469	14	US-10-163-316-3	Sequence 3, Appli
38	2161	40.9	4307	13	US-10-358-283-31	Sequence 31, Appl
39	2161	40.9	4307	16	US-10-191-997-121	Sequence 121, App
40	2156	40.8	4192	15	US-10-247-685-1	Sequence 1, Appli
41	2149	40.6	4407	10	US-09-946-374-316	Sequence 316, App
42	2149	40.6	4407	12	US-10-015-395A-316	Sequence 316, App
43	2149	40.6	4407	13	US-10-206-915-351	Sequence 351, App
44	2149	40.6	4407	13	US-10-199-670-351	Sequence 351, App
45	2149	40.6	4407	13	US-10-201-858-351	Sequence 351, App

ALIGNMENTS

RESULT 1
US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (466)..(3366)
; OTHER INFORMATION:
US-09-989-687-125

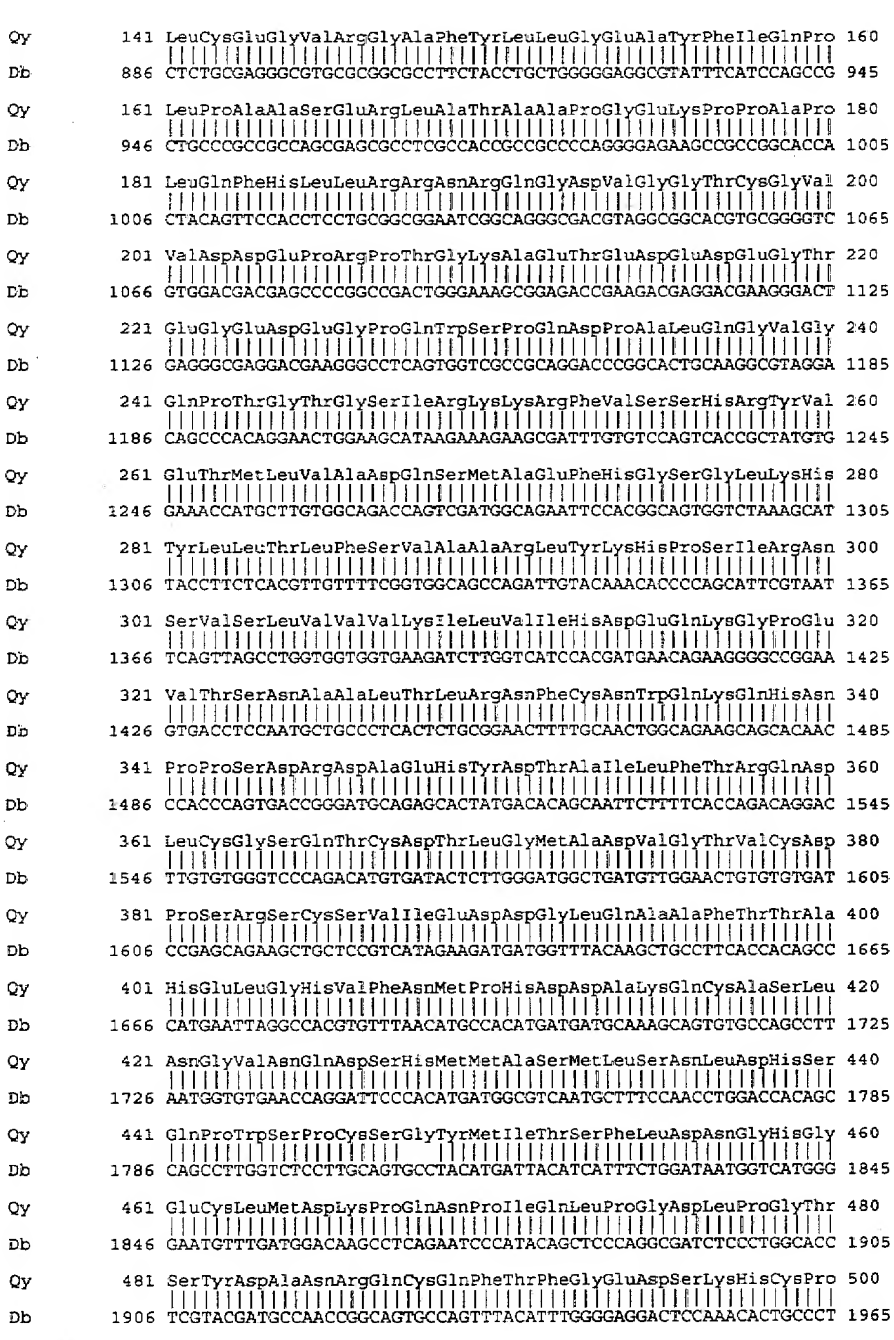
Alignment Scores:

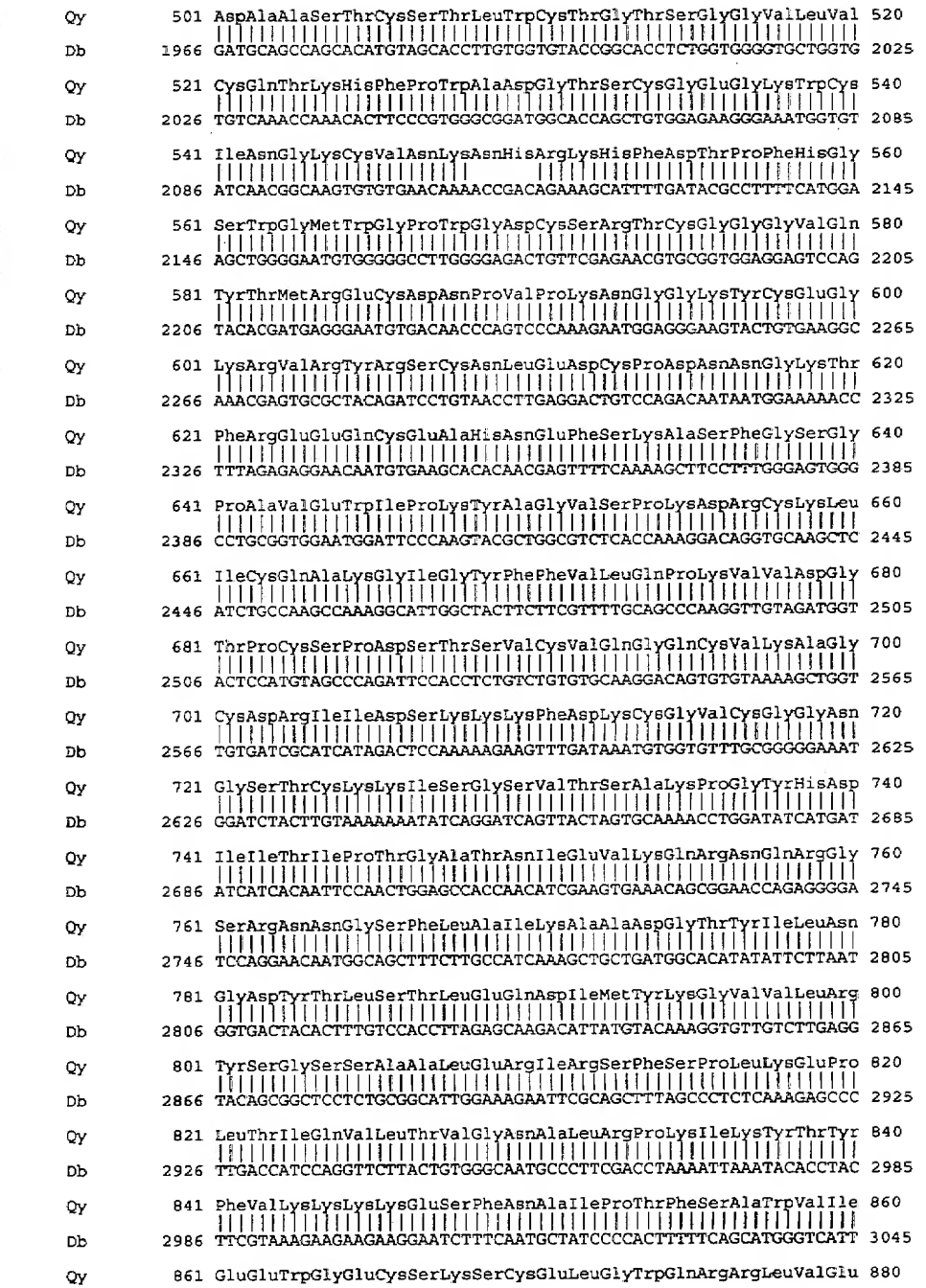
Pred. No.:	0	Length:	4014
Score:	5287.00	Matches:	967
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-373-658C-126 (1-967) x US-09-989-687-125 (1-4014)

```
Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 525

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 585

Qy         41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 645

Qy         61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GTGGTGCCCGGAGCTGGAGCGCGTCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 705

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TTTGACCAGCAGCTGGATCTGGACGTGCCGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 765

Qy        101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGACACCCCGCTTCCGGAAACCGACCTG 825

Qy        121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 885

Qy        141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 945

Qy        161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 1005

Qy        181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACGTGCGGGGTC 1065

Qy        201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 1125

Qy        221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 1185

Qy        241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1245

Qy        261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1305

Qy        281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1365

Qy        301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCCGAA 1425

Qy        321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1485

Qy        341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1545

Qy        361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1605

Qy        381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1606 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1665

Qy        401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1666 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1725

Qy        421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1785

Qy        441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1786 CAGCCTTGGTCTCCTTGCAGTGGCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1845

Qy        461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1905

Qy        481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1906 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCT 1965

Qy        501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 2025

Qy        521 CysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2026 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 2085

Qy        541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 ATCAACGGCAAGTGTGTGAACAAAAACCACAGAAAGCATTTTGATACGCCTTTTCATGGA 2145

Qy        561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2146 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 2205

Qy        581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 2265

Qy        601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 2325

Qy        621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2385

Qy        641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2445

Qy        661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2505
```

```
Qy        681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db       2506 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2565

Qy        701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db       2566 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2625

Qy        721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db       2626 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2685

Qy        741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db       2686 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2745

Qy        761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db       2746 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2805

Qy        781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db       2806 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2865

Qy        801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db       2866 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2925

Qy        821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db       2926 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2985

Qy        841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db       2986 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 3045

Qy        861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db       3046 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 3105

Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db       3106 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 3165

Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db       3166 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 3225

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db       3226 TCTAAGACCTGTGGGAAGGGTTACAAAAAAACAAGCTTGAAGTGTCTGTCCCATGATGGA 3285

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db       3286 GGGGTGTTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 3345

Qy        961 CysThrMetAlaGluCysSer 967
Db       3346 TGCACAATGGCAGAATGCAGT 3366

RESULT 2
US-10-115-286-1
; Sequence 1, Application US/10115286
; Publication No. US20030166065A1
;   GENERAL INFORMATION:
;        APPLICANT: Jonak, Zdenka
;                   Trulli, Stephen
;                   Fornwald, James
;                   Terrett, Jonathan
;                   Hasting, Gregg
;        TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Ratner & Prestia
;             STREET: Box 980
;             CITY: Valley Forge
;             STATE: PA
;             COUNTRY: USA
;             ZIP: 19482
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/115,286
;             FILING DATE: 04-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/845,496
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Prestia, Paul F
;             REGISTRATION NUMBER: 23,031
;             REFERENCE/DOCKET NUMBER: GH-70000
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 610-407-0700
;             TELEFAX: 610-407-0701
;             TELEX: 846169
;    INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4014 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-115-286-1

Alignment Scores:
Pred. No.:                0                Length:          4014
Score:                    5232.00          Matches:         957
Percent Similarity:       99.38%           Conservative:    4
Best Local Similarity:    98.97%           Mismatches:      6
Query Match:              98.96%           Indels:          0
DB:                       15               Gaps:            0

US-09-373-658C-126 (1-967) x US-10-115-286-1 (1-4014)

Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db        466 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 525

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db        526 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 585

Qy         41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db        586 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 645

Qy         61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db        646 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 705

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db        706 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 765

Qy        101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db        766 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 825

Qy        121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db        826 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 885
```


Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 886 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 945
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 946 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 1005
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 1006 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACGTGCGGGGTC 1065
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1066 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 1125
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1126 GAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 1185
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 1186 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1245
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1246 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1305
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1306 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1365
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1366 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1425
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1426 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1485
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1486 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1545
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1546 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1605
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1606 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1665
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1666 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1725
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1726 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1785
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1786 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1845
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1846 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1905
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1906 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCT 1965


Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1966 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 2025
Qy 521 CysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 2026 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 2085
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 2086 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGGA 2145
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
Db 2146 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 2205
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 2206 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 2265
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 2266 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 2325
Qy 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2326 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2385
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2386 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2445
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2446 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2505
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 2506 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2565
Qy 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2566 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2625
Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2626 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2685
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2686 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2745
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2746 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2805
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2806 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2865
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2866 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2925
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2926 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2985
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2986 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 3045
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880

```
Db       3046 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 3105

Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900

Db       3106 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 3165

Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920

Db       3166 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 3225

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940

Db       3226 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 3285

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960

Db       3286 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 3345

Qy        961 CysThrMetAlaGluCysSer 967

Db       3346 TGCACAATGGCAGAATGCAGT 3366

RESULT 3
US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
;  APPLICANT: Holtzman, Douglas A.
;  APPLICANT:  Goodearl, Andrew D.J.
;  TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
;  FILE REFERENCE: 09404/041001
;  CURRENT APPLICATION NUMBER: US/10/105,929
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
;  PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
;  PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 4676
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (460)...(3360)
US-10-105-929-1

Alignment Scores:
Pred. No.:              0           Length:          4676
Score:                  5232.00     Matches:         957
Percent Similarity:     99.38%      Conservative:    4
Best Local Similarity:  98.97%      Mismatches:      6
Query Match:            98.96%      Indels:          0
DB:                     14          Gaps:            0

US-09-373-658C-126 (1-967) x US-10-105-929-1 (1-4676)

Qy           1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20

Db         460 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 519

Qy          21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40

Db         520 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 579

Qy          41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60

Db         580 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 639

Qy          61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80

Db         640 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 699

Qy          81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100

Db         700 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 759

Qy         101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120

Db         760 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 819

Qy         121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140

Db         820 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 879

Qy         141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160

Db         880 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 939

Qy         161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180

Db         940 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 999

Qy         181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200

Db        1000 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACGTGCGGGGTC 1059

Qy         201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220

Db        1060 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 1119

Qy         221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240

Db        1120 GAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 1179

Qy         241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260

Db        1180 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1239

Qy         261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280

Db        1240 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1299

Qy         281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300

Db        1300 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1359

Qy         301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320

Db        1360 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1419

Qy         321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340

Db        1420 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1479

Qy         341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360

Db        1480 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1539

Qy         361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380

Db        1540 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1599

Qy         381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400

Db        1600 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1659

Qy         401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420

Db        1660 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1719

Qy         421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
```

```
Db       1720 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1779

Qy        441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460

Db       1780 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1839

Qy        461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480

Db       1840 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1899

Qy        481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500

Db       1900 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1959

Qy        501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520

Db       1960 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 2019

Qy        521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540

Db       2020 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 2079

Qy        541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560

Db       2080 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGGA 2139

Qy        561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580

Db       2140 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 2199

Qy        581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600

Db       2200 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 2259

Qy        601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620

Db       2260 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 2319

Qy        621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640

Db       2320 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2379

Qy        641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660

Db       2380 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2439

Qy        661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680

Db       2440 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2499

Qy        681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700

Db       2500 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2559

Qy        701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720

Db       2560 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2619

Qy        721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740

Db       2620 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2679

Qy        741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760

Db       2680 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2739

Qy        761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780

Db       2740 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2799

Qy        781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800

Db       2800 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2859

Qy        801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820

Db       2860 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2919

Qy        821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840

Db       2920 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2979

Qy        841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860

Db       2980 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 3039

Qy        861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880

Db       3040 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 3099

Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900

Db       3100 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 3159

Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920

Db       3160 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 3219

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940

Db       3220 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 3279

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960

Db       3280 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 3339

Qy        961 CysThrMetAlaGluCysSer 967

Db       3340 TGCACAATGGCAGAATGCAGT 3360
```

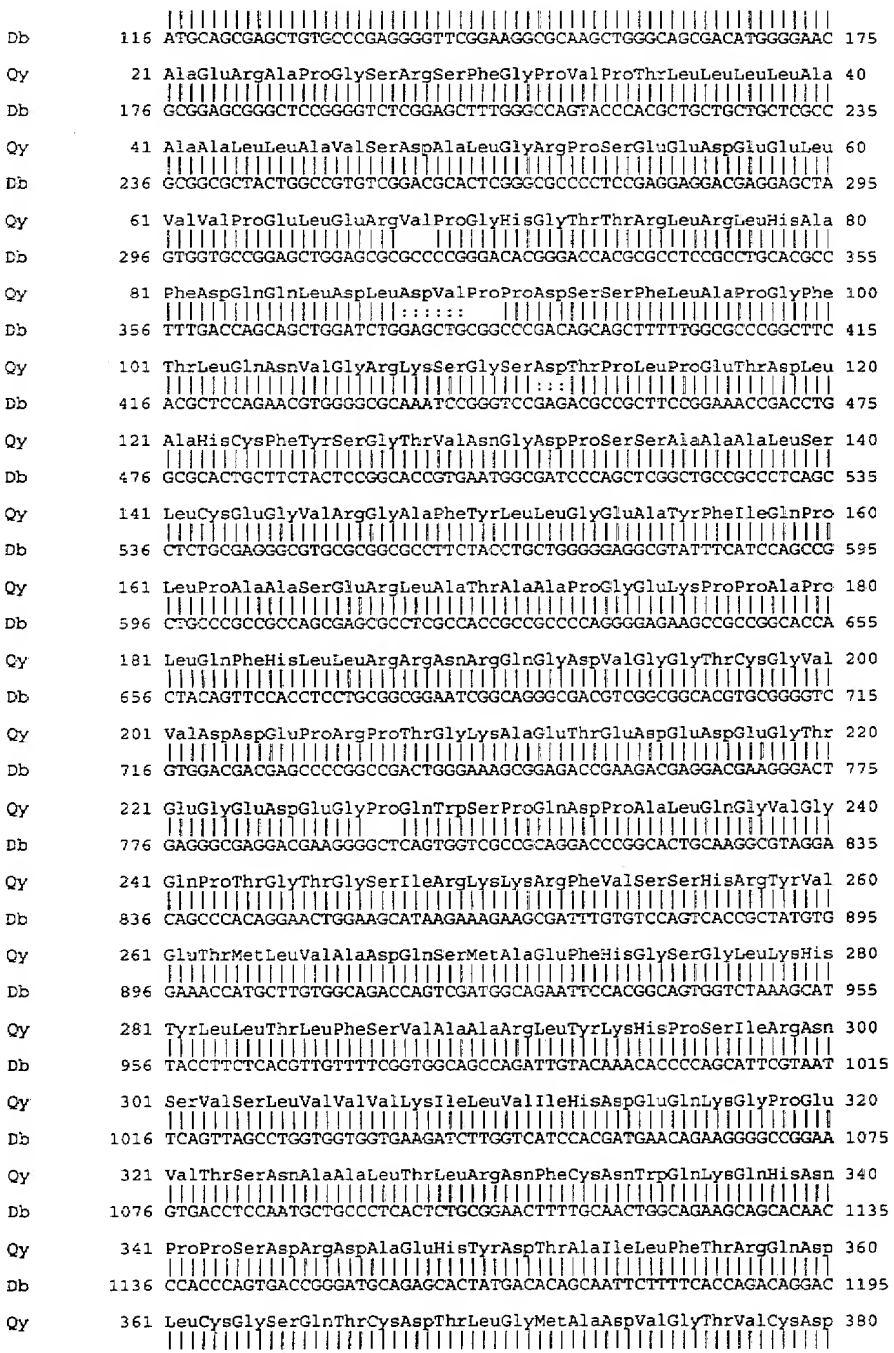
RESULT 4
US-10-210-120-57
; Sequence 57, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 4309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-57

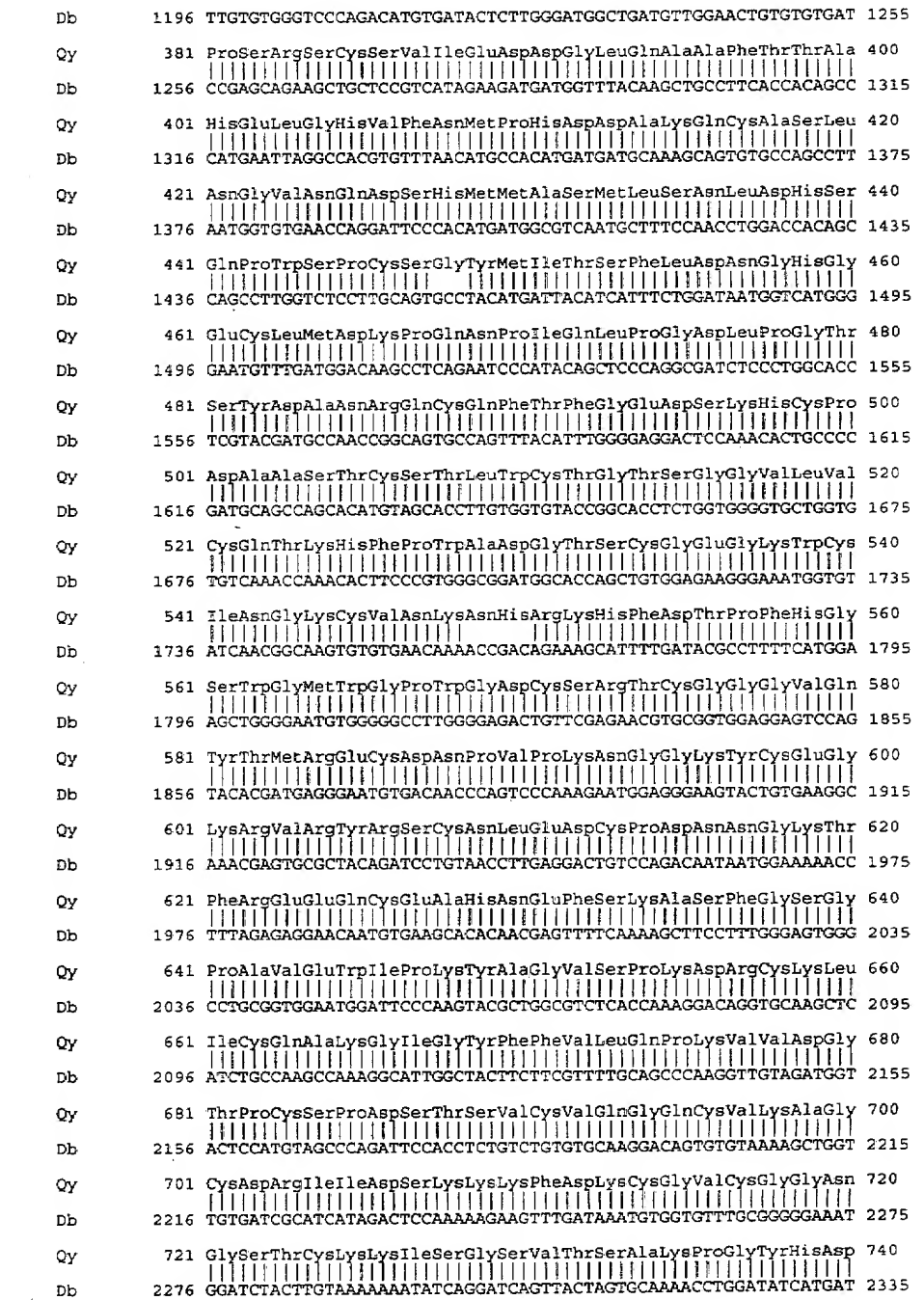
Alignment Scores:

Pred. No.:	0	Length:	4309
Score:	5224.00	Matches:	956
Percent Similarity:	99.28%	Conservative:	4
Best Local Similarity:	98.86%	Mismatches:	7
Query Match:	98.81%	Indels:	0
DB:	15	Gaps:	0

US-09-373-658C-126 (1-967) x US-10-210-120-57 (1-4309)

```
Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
```


Db 116 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 175
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db 176 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCAGTACCCACGCTGCTGCTGCTCGCC 235
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db 236 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 295
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 296 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 355
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 356 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 415
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 416 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 475
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db 476 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 535
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 536 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 595
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 596 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 655
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 656 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACGTGCGGGGTC 715
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 716 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 775
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 776 GAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 835
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 836 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 895
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 896 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 955
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 956 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1015
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1016 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1075
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1076 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1135
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1136 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1195
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380


Db 1196 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1255
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1256 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1315
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1316 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1375
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1376 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1435
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1436 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1495
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1496 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1555
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1556 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1615
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1616 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 1675
Qy 521 CysGlnThrLysHisProProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 1676 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 1735
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 1736 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGGA 1795
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
Db 1796 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 1855
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 1856 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 1915
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 1916 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 1975
Qy 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 1976 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2035
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2036 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2095
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2096 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2155
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 2156 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2215
Qy 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2216 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2275
Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2276 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2335

```
Qy        741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2395

Qy        761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2455

Qy        781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2515

Qy        801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2575

Qy        821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2576 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2635

Qy        841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2636 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 2695

Qy        861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2696 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGACGAAGACTGGTAGAA 2755

Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2756 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 2815

Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2816 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 2875

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db       2876 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 2935

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       2936 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 2995

Qy        961 CysThrMetAlaGluCysSer 967
              |||||||||||||||||||||
Db       2996 TGCACAATGGCAGAATGCAGT 3016
```

```
RESULT 5
US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
;  APPLICANT: Khan, Javed
;  APPLICANT:  Ringner, Markus
;  APPLICANT:  Peterson, Carsten
;  APPLICANT:  Meltzer, Paul
;  TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
;  TITLE OF INVENTION:  DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
;  FILE REFERENCE: 11613.56USI1
;  CURRENT APPLICATION NUMBER: US/10/159,563
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 10/133,937
;  PRIOR FILING DATE: 2002-04-25
;  NUMBER OF SEQ ID NOS: 444
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
;   LENGTH: 4459
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-159-563-192
```

Alignment Scores:

Pred. No.:	0	Length:	4459
Score:	5224.00	Matches:	956
Percent Similarity:	99.28%	Conservative:	4
Best Local Similarity:	98.86%	Mismatches:	7
Query Match:	98.81%	Indels:	0
DB:	16	Gaps:	0

US-09-373-658C-126 (1-967) x US-10-159-563-192 (1-4459)

```
Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 302

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 362

Qy         41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 422

Qy         61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
              ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        423 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 482

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
              ||||||||||||||||||::::::    ||||||||||||||||||||||||||||||||||||
Db        483 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 542

Qy        101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db        543 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 602

Qy        121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 662

Qy        141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 722

Qy        161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 782

Qy        181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACGTGCGGGGTC 842

Qy        201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 902

Qy        221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        903 GAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 962

Qy        241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1022

Qy        261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1082

Qy        281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1142

Qy        301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1202
```

```
Qy        321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db       1203 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1262

Qy        341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db       1263 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1322

Qy        361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db       1323 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1382

Qy        381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db       1383 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1442

Qy        401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db       1443 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1502

Qy        421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db       1503 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1562

Qy        441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db       1563 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1622

Qy        461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db       1623 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1682

Qy        481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db       1683 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1742

Qy        501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db       1743 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 1802

Qy        521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db       1803 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 1862

Qy        541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db       1863 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGGA 1922

Qy        561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
Db       1923 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 1982

Qy        581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db       1983 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 2042

Qy        601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db       2043 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 2102

Qy        621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db       2103 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2162

Qy        641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db       2163 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2222

Qy        661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db       2223 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2282

Qy        681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db       2283 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2342

Qy        701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db       2343 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2402

Qy        721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db       2403 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2462

Qy        741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db       2463 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2522

Qy        761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db       2523 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2582

Qy        781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db       2583 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2642

Qy        801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db       2643 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2702

Qy        821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db       2703 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2762

Qy        841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db       2763 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 2822

Qy        861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db       2823 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 2882

Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db       2883 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 2942

Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db       2943 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 3002

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db       3003 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 3062

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db       3063 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 3122

Qy        961 CysThrMetAlaGluCysSer 967
Db       3123 TGCACAATGGCAGAATGCAGT 3143
```

RESULT 6
US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56USI1
; CURRENT APPLICATION NUMBER: US/10/159,563

; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-308

Alignment Scores:

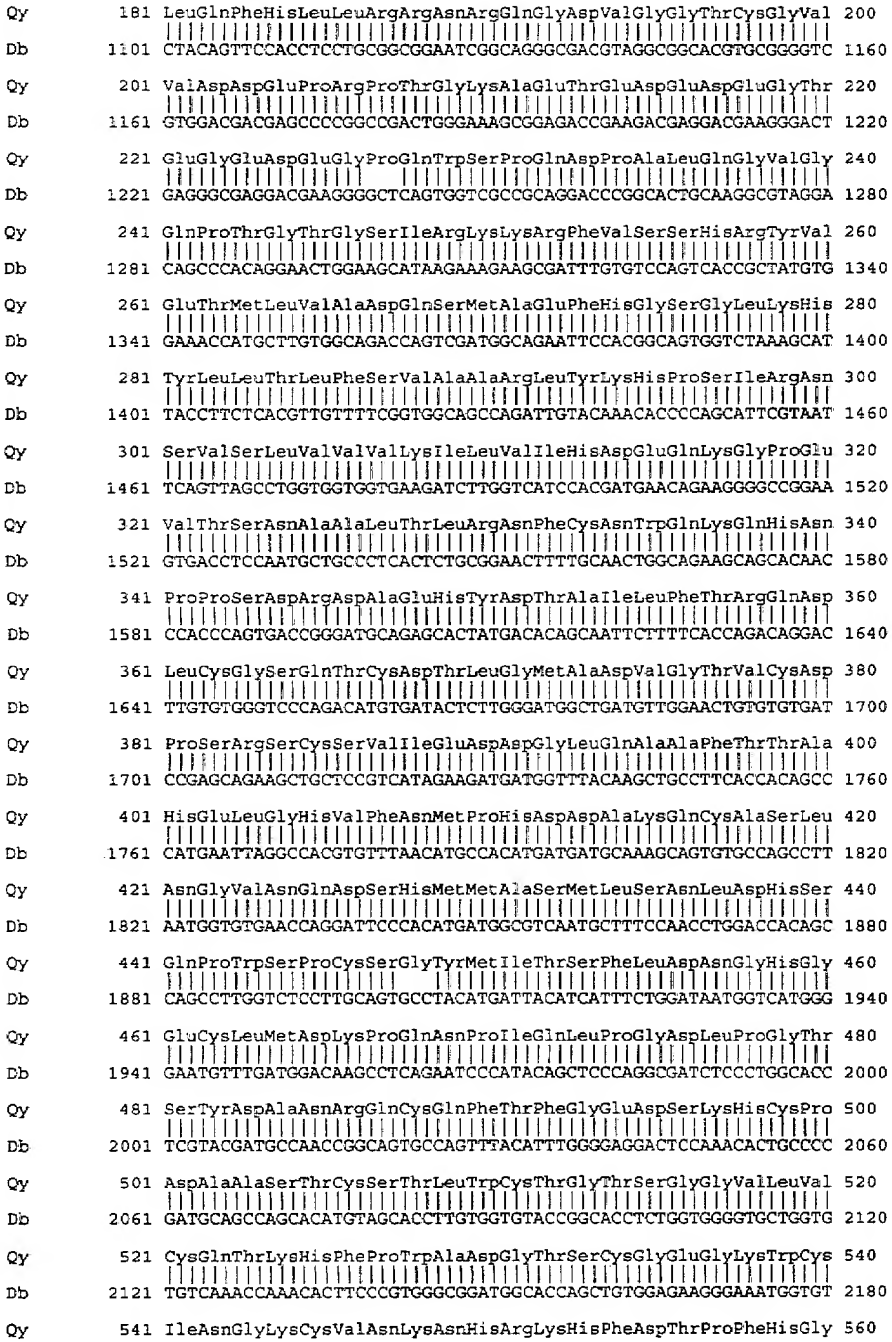
Pred. No.:	0	Length:	4459
Score:	5224.00	Matches:	956
Percent Similarity:	99.28%	Conservative:	4
Best Local Similarity:	98.86%	Mismatches:	7
Query Match:	98.81%	Indels:	0
DB:	16	Gaps:	0

US-09-373-658C-126 (1-967) x US-10-159-563-308 (1-4459)

```
Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 302

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 362

Qy         41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 422

Qy         61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        423 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 482

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
              ||||||||||||||||||::::::  ||||||||||||||||||||||||||||||||||
Db        483 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 542

Qy        101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
              ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db        543 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 602

Qy        121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 662

Qy        141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 722

Qy        161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 782

Qy        181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTCGGCGGCACGTGCGGGGTC 842

Qy        201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 902

Qy        221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        903 GAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 962

Qy        241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1022

Qy        261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1082

Qy        281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1142

Qy        301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1202

Qy        321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1262

Qy        341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1322

Qy        361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1382

Qy        381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1442

Qy        401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1502

Qy        421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1562

Qy        441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1563 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1622

Qy        461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 1682

Qy        481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1742

Qy        501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 1802

Qy        521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 1862

Qy        541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1863 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGGA 1922

Qy        561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1923 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 1982

Qy        581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 2042

Qy        601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2043 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 2102

Qy        621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
```

```
Db       2103 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2162

Qy        641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db       2163 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2222

Qy        661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db       2223 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2282

Qy        681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db       2283 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2342

Qy        701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db       2343 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2402

Qy        721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db       2403 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2462

Qy        741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db       2463 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2522

Qy        761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db       2523 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2582

Qy        781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db       2583 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2642

Qy        801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db       2643 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 2702

Qy        821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db       2703 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 2762

Qy        841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db       2763 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 2822

Qy        861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db       2823 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 2882

Qy        881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db       2883 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 2942

Qy        901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db       2943 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 3002

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db       3003 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 3062

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db       3063 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 3122

Qy        961 CysThrMetAlaGluCysSer 967
Db       3123 TGCACAATGGCAGAATGCAGT 3143

RESULT 7
US-09-971-429B-17
```

```
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
;  APPLICANT: Lasek, Amy K. W.
;  APPLICANT:  Shyjan, Andrew W.
;  APPLICANT:  Turner, Christopher M.
;  TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
;  FILE REFERENCE: PA-0040 US
;  CURRENT APPLICATION NUMBER: US/09/971,429B
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/239,024
;  PRIOR FILING DATE: 2000-04-10
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PERL Program
; SEQ ID NO 17
;   LENGTH: 4760
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 118
;   OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17

Alignment Scores:
Pred. No.:                0                Length:          4760
Score:                    5224.00          Matches:         956
Percent Similarity:       99.28%           Conservative:    4
Best Local Similarity:    98.86%           Mismatches:      7
Query Match:              98.81%           Indels:          0
DB:                       10               Gaps:            0

US-09-373-658C-126 (1-967) x US-09-971-429B-17 (1-4760)

Qy           1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db         561 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 620

Qy          21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db         621 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCAGTACCCACGCTGCTGCTGCTCGCC 680

Qy          41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db         681 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 740

Qy          61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db         741 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 800

Qy          81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db         801 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 860

Qy         101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db         861 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 920

Qy         121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db         921 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 980

Qy         141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db         981 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 1040

Qy         161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db        1041 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 1100
```


Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 1101 CTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACGTGCGGGGTC 1160
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1161 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 1220
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1221 GAGGGCGAGGACGAAGGGGCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 1280
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 1281 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1340
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1341 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1400
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1401 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1460
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1461 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1520
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1521 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1580
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1581 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1640
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1641 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1700
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1701 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1760
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1761 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1820
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1821 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1880
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1881 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1940
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1941 GAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTCCCTGGCACC 2000
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 2001 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 2060
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 2061 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 2120
Qy 521 CysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 2121 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 2180
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 2181 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCTTTTCATGGA 2240
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
Db 2241 AGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAG 2300
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 2301 TACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGC 2360
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 2361 AAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACC 2420
Qy 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2421 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2480
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2481 CCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTC 2540
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2541 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGT 2600
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 2601 ACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT 2660
Qy 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2661 TGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGCGGGGGAAAT 2720
Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2721 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2780
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2781 ATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCAGAGGGGA 2840
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2841 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATATATTCTTAAT 2900
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2901 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTTGTCTTGAGG 2960
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2961 TACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC 3020
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 3021 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAATACACCTAC 3080
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 3081 TTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCATT 3140
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3141 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAA 3200
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3201 TGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGC 3260
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920

```
Db       3261 ACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGT 3320

Qy        921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3321 TCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGA 3380

Qy        941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db       3381 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTT 3440

Qy        961 CysThrMetAlaGluCysSer 967
              |||||||||||||||||||||
Db       3441 TGCACAATGGCAGAATGCAGT 3461

RESULT 8
US-09-373-658-1
; Sequence 1, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
;  APPLICANT: Iruela-Arispe, Luisa
;  APPLICANT:  Hastings, Gregg A.
;  APPLICANT:  Ruben, Steven M.
;  APPLICANT:  Jonak, Zdenka L.
;  APPLICANT:  Trulli, Stephen H.
;  APPLICANT:  Fronwald, James A.
;  APPLICANT:  Terrett, Jonathan A.
;  TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
;  FILE REFERENCE: 1488.1070006
;  CURRENT APPLICATION NUMBER: US/09/373,658
;  CURRENT FILING DATE:  1999-08-13
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3261
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2853)
;   NAME/KEY: UNSURE
;   LOCATION: (3095)
;   OTHER INFORMATION: May be any nucleic acid
;   NAME/KEY: UNSURE
;   LOCATION: (3248)
;   OTHER INFORMATION: May be any nucleic acid
;   NAME/KEY: UNSURE
;   LOCATION: (3255)
;   OTHER INFORMATION: May be any nucleic acid
;   NAME/KEY: UNSURE
;   LOCATION: (3261)
;   OTHER INFORMATION: May be any nucleic acid
US-09-373-658-1

Alignment Scores:
Pred. No.:                0              Length:          3261
Score:                    5144.00        Matches:         940
Percent Similarity:       99.37%         Conservative:    4
Best Local Similarity:    98.95%         Mismatches:      6
Query Match:              97.30%         Indels:          0
DB:                       10             Gaps:            0

US-09-373-658C-126 (1-967) x US-09-373-658-1 (1-3261)

Qy          18 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 37
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 60

Qy          38 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 120

Qy          58 GluGluLeuValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArg 77
               ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||

Db         121 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 180

Qy          78 LeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAla 97
               ||||||||||||||||||||||||||||||||||||:::::  ||||||||||||||||||||
Db         181 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 240

Qy          98 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGlu 117
               ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db         241 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 300

Qy         118 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 360

Qy         138 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 157
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 420

Qy         158 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 480

Qy         178 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 540

Qy         198 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 217
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 600

Qy         218 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 237
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 660

Qy         238 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 720

Qy         258 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 277
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 780

Qy         278 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 297
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 840

Qy         298 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 900

Qy         318 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 337
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 960

Qy         338 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 357
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1020

Qy         358 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 377
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1080

Qy         378 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 397
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1140

Qy         398 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 417
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1200

Qy         418 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 437
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1260
```

```
Qy        438 AspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsn 457
Db       1261 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1320

Qy        458 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 477
Db       1321 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1380

Qy        478 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 497
Db       1381 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1440

Qy        498 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 517
Db       1441 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1500

Qy        518 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 537
Db       1501 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1560

Qy        538 LysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrPro 557
Db       1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 1620

Qy        558 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 577
Db       1621 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1680

Qy        578 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 597
Db       1681 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 1740

Qy        598 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 617
Db       1741 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 1800

Qy        618 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 637
Db       1801 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 1860

Qy        638 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 657
Db       1861 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 1920

Qy        658 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 677
Db       1921 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 1980

Qy        678 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 697
Db       1981 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040

Qy        698 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 717
Db       2041 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2100

Qy        718 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 737
Db       2101 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2160

Qy        738 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 757
Db       2161 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2220

Qy        758 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 777
Db       2221 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2280

Qy        778 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 797
Db       2281 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2340

Qy        798 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 817
Db       2341 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2400

Qy        818 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 837
Db       2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2460

Qy        838 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 857
Db       2461 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520

Qy        858 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 877
Db       2521 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2580

Qy        878 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 897
Db       2581 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2640

Qy        898 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 917
Db       2641 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2700

Qy        918 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSer 937
Db       2701 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 2760

Qy        938 HisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPhe 957
Db       2761 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 2820

Qy        958 IleAspPheCysThrMetAlaGluCysSer 967
Db       2821 ATAGACTTTTGCACAATGGCAGAATGCAGT 2850
```

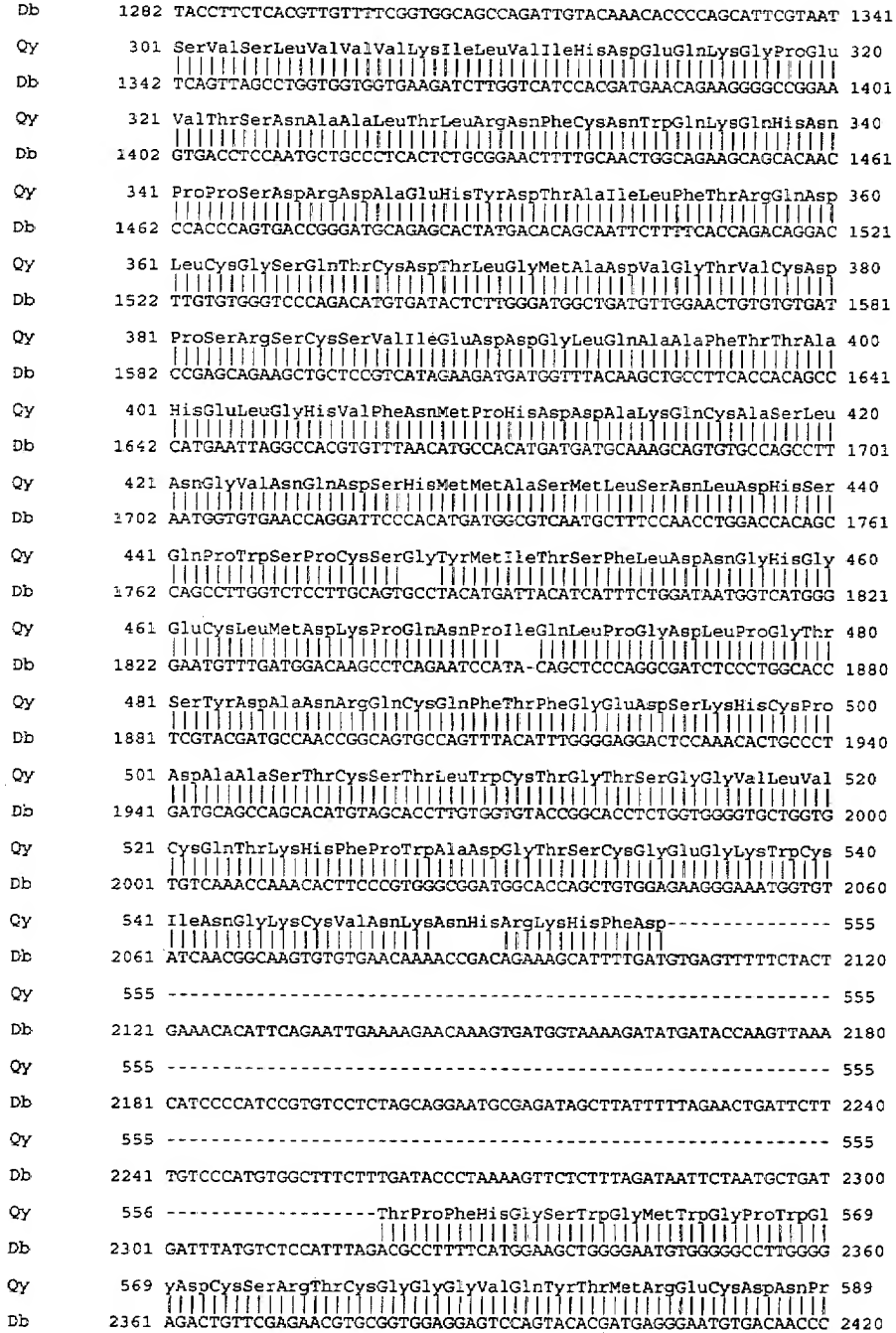
RESULT 9
US-09-989-687-1
; Sequence 1, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2853)
; NAME/KEY: misc_feature
; LOCATION: (3195)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (3248)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (3255)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (3261)
; OTHER INFORMATION: n is any nucleic acid
US-09-989-687-1

Alignment Scores:

Pred. No.:	0	Length:	3261
Score:	5144.00	Matches:	940

```
Percent Similarity:      99.37%          Conservative:   4
Best Local Similarity:   98.95%          Mismatches:     6
Query Match:             97.30%          Indels:         0
DB:                      11              Gaps:           0

US-09-373-658C-126 (1-967) x US-09-989-687-1 (1-3261)

Qy        18 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 37
Db         1 ATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 60

Qy        38 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57
Db        61 CTGCTCGCCGCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGAC 120

Qy        58 GluGluLeuValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArg 77
Db       121 GAGGAGCTAGTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGC 180

Qy        78 LeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAla 97
Db       181 CTGCACGCCTTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCG 240

Qy        98 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGlu 117
Db       241 CCCGGCTTCACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAA 300

Qy       118 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 137
Db       301 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCC 360

Qy       138 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 157
Db       361 GCCCTCAGCCTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTC 420

Qy       158 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 177
Db       421 ATCCAGCCGCTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCG 480

Qy       178 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 197
Db       481 CCGGCACCACTACAGTTCCACCTCCTGCGGCGGAATCGGCAGGGCGACGTAGGCGGCACG 540

Qy       198 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 217
Db       541 TGCGGGGTCGTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGAC 600

Qy       218 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 237
Db       601 GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAA 660

Qy       238 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 257
Db       661 GGCGTAGGACAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCAC 720

Qy       258 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 277
Db       721 CGCTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGT 780

Qy       278 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 297
Db       781 CTAAAGCATTACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGC 840

Qy       298 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 317
Db       841 ATTCGTAATTCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 900

Qy       318 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 337
Db       901 GGGCCGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAG 960

Qy       338 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 357

Db       961 CAGCACAACCCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACC 1020

Qy       358 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 377
Db      1021 AGACAGGACTTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACT 1080

Qy       378 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 397
Db      1081 GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTC 1140

Qy       398 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 417
Db      1141 ACCACAGCCCATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGT 1200

Qy       418 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 437
Db      1201 GCCAGCCTTAATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTG 1260

Qy       438 AspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsn 457
Db      1261 GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAT 1320

Qy       458 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 477
Db      1321 GGTCATGGGGAATGTTTGATGGACAAGCCTCAGAATCCCATACAGCTCCCAGGCGATCTC 1380

Qy       478 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 497
Db      1381 CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA 1440

Qy       498 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 517
Db      1441 CACTGCCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGG 1500

Qy       518 ValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSerCysGlyGluGly 537
Db      1501 GTGCTGGTGTGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGG 1560

Qy       538 LysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrPro 557
Db      1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATACGCCT 1620

Qy       558 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 577
Db      1621 TTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1680

Qy       578 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 597
Db      1681 GGAGTCCAGTACACGATGAGGGAATGTGACAACCCAGTCCCAAAGAATGGAGGGAAGTAC 1740

Qy       598 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 617
Db      1741 TGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAACCTTGAGGACTGTCCAGACAATAAT 1800

Qy       618 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 637
Db      1801 GGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTT 1860

Qy       638 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 657
Db      1861 GGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTACGCTGGCGTCTCACCAAAGGACAGG 1920

Qy       658 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 677
Db      1921 TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTGCAGCCCAAGGTT 1980

Qy       678 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 697
Db      1981 GTAGATGGTACTCCATGTAGCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040

Qy       698 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 717
Db      2041 AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGAAGTTTGATAAATGTGGTGTTTGC 2100
```

```
Qy        718 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GGGGGAAATGGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2160

Qy        738 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TATCATGATATCATCACAATTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2220

Qy        758 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT 2280

Qy        778 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTT 2340

Qy        798 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGAAAGAATTCGCAGCTTTAGCCCTCTC 2400

Qy        818 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA 2460

Qy        838 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TACACCTACTTCGTAAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520

Qy        858 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTGGGTTGGCAGAGAAGA 2580

Qy        878 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCAAAGGAAGTGAAG 2640

Qy        898 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2700

Qy        918 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSer 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAAGAAGCTTGAAGTGTCTGTCC 2760

Qy        938 HisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPhe 957
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db       2761 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTC 2820

Qy        958 IleAspPheCysThrMetAlaGluCysSer 967
              |||||||||||||||||||||||||||||
Db       2821 ATAGACTTTTGCACAATGGCAGAATGCAGT 2850

RESULT 10
US-10-425-114-26851
; Sequence 26851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26851
;   LENGTH: 4848
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4654-036-D4_FLI
US-10-425-114-26851

Alignment Scores:
Pred. No.:                0                Length:              4848
Score:                    5140.50          Matches:             956
Percent Similarity:       92.40%           Conservative:        4
Best Local Similarity:    92.01%           Mismatches:          7
Query Match:              97.23%           Indels:              73
DB:                       13               Gaps:                1

US-09-373-658C-126 (1-967) x US-10-425-114-26851 (1-4848)

Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGGCGCAAGCTGGGCAGCGACATGGGGAAC 501

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTGCTGCTCGCC 561

Qy         41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GCGGCGCTACTGGCCGTGTCGGACGCACTCGGGCGCCCCTCCGAGGAGGACGAGGAGCTA 621

Qy         61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 GTGGTGCCGGAGCTGGAGCGCGCCCCGGGACACGGGACCACGCGCCTCCGCCTGCACGCC 681

Qy         81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
              ||||||||||||||||||||:::::: ||||||||||||||||||||||||||||||||||
Db        682 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTTGGCGCCCGGCTTC 741

Qy        101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        742 ACGCTCCAGAACGTGGGGCGCAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 801

Qy        121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCCAGCTCGGCTGCCGCCCTCAGC 861

Qy        141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 CTCTGCGAGGGCGTGCGCGGCGCCTTCTACCTGCTGGGGGAGGCGTATTTCATCCAGCCG 921

Qy        161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 CTGCCCGCCGCCAGCGAGCGCCTCGCCACCGCCGCCCCAGGGGAGAAGCCGCCGGCACCA 981

Qy        181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 CTACAGTTCCACCTCCTGCGGCCGGAATCGGCAGGGCGACGTAGGCGGCACGTGCGGGGTG 1041

Qy        201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 GTGGACGACGAGCCCCGGCCGACTGGGAAAGCGGAGACCGAAGACGAGGACGAAGGGACT 1101

Qy        221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 GAGGGCGAGGACGAAGGGCCTCAGTGGTCGCCGCAGGACCCGGCACTGCAAGGCGTAGGA 1161

Qy        241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 CAGCCCACAGGAACTGGAAGCATAAGAAAGAAGCGATTTGTGTCCAGTCACCGCTATGTG 1221

Qy        261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCAT 1281

Qy        281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```


Db 1282 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAAT 1341
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1342 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAA 1401
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1402 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAAC 1461
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1462 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCTTTTCACCAGACAGGAC 1521
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1522 TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1581
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1582 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCTTCACCACAGCC 1641
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1642 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAAGCAGTGTGCCAGCCTT 1701
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1702 AATGGTGTGAACCAGGATTCCCACATGATGGCGTCAATGCTTTCCAACCTGGACCACAGC 1761
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1762 CAGCCTTGGTCTCCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGGG 1821
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1822 GAATGTTTGATGGACAAGCCTCAGAATCCATA-CAGCTCCCAGGCGATCTCCCTGGCACC 1880
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1881 TCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCT 1940
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1941 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGCTGGTG 2000
Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 2001 TGTCAAACCAAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGT 2060
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAsp---------- 555
Db 2061 ATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGATGTGAGTTTTTCTACT 2120
Qy 555 ---------- 555
Db 2121 GAAACACATTCAGAATTGAAAAGAACAAAGTGATGGTAAAAGATATGATACCAAGTTAAA 2180
Qy 555 ---------- 555
Db 2181 CATCCCCATCCGTGTCCTCTAGCAGGAATGCGAGATAGCTTATTTTTAGAACTGATTCTT 2240
Qy 555 ---------- 555
Db 2241 TGTCCCATGTGGCTTTCTTTGATACCCTAAAAGTTCTCTTTAGATAATTCTAATGCTGAT 2300
Qy 556 ----------ThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGl 569
Db 2301 GATTTATGTCTCCATTTAGACGCCTTTTCATGGAAGCTGGGGAATGTGGGGGCCTTGGGG 2360
Qy 569 yAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnPr 589
Db 2361 AGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACAACCC 2420
Qy 589 oValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAs 609
Db 2421 AGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAGATCCTGTAA 2480
Qy 609 nLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHi 629
Db 2481 CCTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATGTGAAGCACA 2540
Qy 629 sAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTy 649
Db 2541 CAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGATTCCCAAGTA 2600
Qy 649 rAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTy 669
Db 2601 CGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTA 2660
Qy 669 rPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSe 689
Db 2661 CTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCAGATTCCACCTC 2720
Qy 689 rValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLy 709
Db 2721 TGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGACTCCAAAAA 2780
Qy 709 sLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGl 729
Db 2781 GAAGTTTGATAAATGTGGTGTTTGCGGGGGAAATGGATCTACTTGTAAAAAAATATCAGG 2840
Qy 729 ySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaTh 749
Db 2841 ATCAGTTACTAGTGCAAAACCTGGATATCATGATATCATCACAATTCCAACTGGAGCCAC 2900
Qy 749 rAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAl 769
Db 2901 CAACATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGC 2960
Qy 769 aIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGl 789
Db 2961 CATCAAAGCTGCTGATGGCACATATATTCTTAATGGTGACTACACTTTGTCCACCTTAGA 3020
Qy 789 uGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGl 809
Db 3021 GCAAGACATTATGTACAAAGGTGTTGTCTTGAGGTACAGCGGCTCCTCTGCGGCATTGGA 3080
Qy 809 uArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGl 829
Db 3081 AAGAATTCGCAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGG 3140
Qy 829 yAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPh 849
Db 3141 CAATGCCCTTCGACCTAAAATTAAATACACCTACTTCGTAAAGAAGAAGAAGGAATCTTT 3200
Qy 849 eAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSe 869
Db 3201 CAATGCTATCCCCACTTTTTCAGCATGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTC 3260
Qy 869 rCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAl 889
Db 3261 ATGTGAATTGGGTTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAGCCTGC 3320
Qy 889 aSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCy 909
Db 3321 TTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGACCATCCCTG 3380
Qy 909 sProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLy 929
Db 3381 CCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAAGGGTTACAA 3440
Qy 929 sLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSerCysAs 949
Db 3441 AAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGCTGTGA 3500

```
Qy        949 pProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
Db       3501 TCCTTTAAAGAAACCTAAACATTTCATAGACTTTTGCACAATGGCAGAATGCAGT 3555
```

RESULT 11
US-10-152-319A-1840
; Sequence 1840, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1840
; LENGTH: 4878
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_024400
US-10-152-319A-1840

Alignment Scores:

Pred. No.:	0	Length:	4878
Score:	4287.00	Matches:	790
Percent Similarity:	87.17%	Conservative:	59
Best Local Similarity:	81.11%	Mismatches:	111
Query Match:	81.09%	Indels:	14
DB:	12	Gaps:	5

US-09-373-658C-126 (1-967) x US-10-152-319A-1840 (1-4878)

```
Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db        395 ATGCAGCCAGAAGTCCCTTTGGGGTCAGGCAAGCTGAAGCCCTGCTCAGACATGGGGAC 454

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db        455 ATCCAGCGGGCAGCGAAGTTTCGGAGCTCTCAGTCTGCACACATGCTGTTGCTACTCCTC 514

Qy         41 AlaAla---------LeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57
Db        515 GCTTCCATAACAATGCTGCTGTGTGTGCGGGGCGCACACGGGCGCCCCACGGAGGAAGAC 574

Qy         58 GluGluLeuValValProGluLeuGluArgValProGlyHis---GlyThrThrArgLeu 76
Db        575 GAGGAGCTGGTGCTGCCCTCGCTGGAGCGCGCCCGGGGCCACGATTCCACCACACTCCTC 634

Qy         77 ArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeu 96
Db        635 CGTCTGGACGCCTTTGGTCAGCAGCTGCATCTGAAGTTGCAGCCAGACAGCGGTTTCTTA 694

Qy         97 AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu--- 115
Db        695 GCGCCTGGCTTCACCCTCCAGACGGTGGGGCGCAGTCCTGGGTCCGAGGCACAGCATCTG 754

Qy        116 ---ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSer 134
Db        755 GACCCCACTGGGGACCTGGCCCACTGCTTCTACTCTGGCACGGTGAACGGTGACCCCAGC 814

Qy        135 SerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGlu 154
Db        815 TCCGCCGCCGCCCTCAGCCTCTGTGAAGGTGTGCGCGGTGCCTTCTACCTACAAGGCGAG 874

Qy        155 AlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThrAlaAlaPro 173
Db        875 GAGTTCTTCATTCAGCCAGCGCCTGCGGTGGCCACCGAGCGCCTGGTCCCCGCCGAACCG 934

Qy        174 GlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAsp 193
Db        935 AAGGAGGAGTCAATCGCACCTCCGCGGTTCCACATCCTGAGGCGAAGGCGGCGGGGCAGC 994

Qy        194 ValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThr 213
Db        995 GGCGGCGCAAAGTGCGGTGTCATGGACGAAGAGACCCTGCCAACC--------------- 1039

Qy        214 GluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAsp 233
Db       1040 ------AGCAACTCGGGTCGCGAAAGCCAGAACACCCCGGACCAGTGGCCTCTGCGGAAC 1093

Qy        234 ProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPhe 253
Db       1094 CCCACTCCTCAGGGCGCGGGAAAGCCAACAGGACCAGGAAGCATAAGGAAGAAGCGATTT 1153

Qy        254 ValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPhe 273
Db       1154 GTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTGGCTGACCAGTCCATGGCTGACTTC 1213

Qy        274 HisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyr 293
Db       1214 CACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTCTCGGTGGCAGCCAGATTTTAC 1273

Qy        294 LysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHis 313
Db       1274 AAGCACCCCAGCATTAGGAATTCAATTAGTCTGGTGGTGGTGAAGATCTTGGTCATATAT 1333

Qy        314 AspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCys 333
Db       1334 GAGGAGCAGAAGGGACCGGAAGTTACTTCCAATGCCGCTCTCACCCTTAGGAATTTCTGT 1393

Qy        334 AsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAla 353
Db       1394 AGCTGGCAGAAACAGCACAACAGCCCCAGTGACCGGGATCCAGAGCACTATGACACAGCG 1453

Qy        354 IleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAla 373
Db       1454 ATTCTGTTCACCAGACAGGATTTATGTGGCTCCCACACCTGTGACACTCTCGGGATGGCT 1513

Qy        374 AspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeu 393
Db       1514 GATGTTGGAACTGTATGTGACCCCAGCAGGAGCTGTTCGGTCATCGAAGATGATGGTTTA 1573

Qy        394 GlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAsp 413
Db       1574 CAGGCTGCCTTCACCACAGCCCATGAATTGGGCCATGTGTTTAACATGCCACACGATGAC 1633

Qy        414 AlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMet 433
```

```
Db       1634 GCCAAGCACTGCGCCAGCTTTAATGGCGTGAGTGGGGATTCCCATCTGATGGCCTCGATG 1693

Qy        434 LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSer 453

Db       1694 CTCTCCAGCTTGGACCACAGCCAGCCCTGGTCTCCTTGCAGTGCCTACATGGTCACATCA 1753

Qy        454 PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeu 473

Db       1754 TTCCTGGACAACGGCCATGGGGAATGTTTGATGGACAAGCCGCAGAACCCAATCAAGCTC 1813

Qy        474 ProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGly 493

Db       1814 CCATCTGATCTTCCCGGTACCTTGTACGATGCCAACCGCCAGTGTCAGTTTACCTTCGGG 1873

Qy        494 GluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGly 513

Db       1874 GAGGAATCCACGCACTGCCCTGATGCAGCCAGCACATGCAGTACCCTGTGGTGCACTGGC 1933

Qy        514 ThrSerGlyGlyValLeuValCysGlnThrLysHisProTrpAlaAspGlyThrSer 533

Db       1934 ACCTCCGGTGGCTTACTGGTGTGCCAAACAAAACACTTCCCTTGGGCAGATGGCACCAGC 1993

Qy        534 CysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHis 553

Db       1994 TGCGGAGAAGGGAAATGGTGTGTCAGCGGCAAGTGTGTGAACAAGACCGACATGAAGCAC 2053

Qy        554 PheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArg 573

Db       2054 TTTGCTACTCCTGTTCATGGGAGCTGGGGACCGTGGGGACCATGGGGAGACTGCTCAAGA 2113

Qy        574 ThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsn 593

Db       2114 ACCTGTGGTGGAGGAGTTCAATATACAATGAGAGAATGTGACAACCCGGTCCCAAAGAAC 2173

Qy        594 GlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCys 613

Db       2174 GGGGGGAAGTACTGCGAAGGCAAACGAGTCCGCTACAGGTCCTGTAACATTGAGGACTGT 2233

Qy        614 ProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSer 633

Db       2234 CCAGACAATAACGGAAAAACATTCAGAGAGGAGCAATGCGAGGCGCACAATGAGTTTTCC 2293

Qy        634 LysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSer 653

Db       2294 AAAGCTTCCTTTGGGAATGAACCCACGGTGGAATGGACACCCAAGTATGCTGGCGTCTCG 2353

Qy        654 ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeu 673

Db       2354 CCAAAGGACAGGTGCAAGCTTACCTGCGAAGCCAAAGGCATTGGCTACTTCTTTGTTTTA 2413

Qy        674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693

Db       2414 CAGCCCAAGGTGGTAGATGGCACTCCCTGTAGTCCAGACTCTACTTCTGTCTGTGTGCAA 2473

Qy        694 GlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLys 713

Db       2474 GGACAGTGTGTGAAAGCTGGCTGTGATCGCATCATAGACTCCAAAAAGAAGTTCGATAAG 2533

Qy        714 CysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSer 733

Db       2534 TGTGGCGTTTGTGGAGGAAATGGCTCCACGTGCAAGAAAATATCAGGAACGGTCACTAGT 2593

Qy        734 AlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluVal 753

Db       2594 ACAAGACCTGGGTATCATGACATTGTCACAATTCCTGCTGGAGCCACCAACATTGAAGTG 2653

Qy        754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAla 773

Db       2654 AAACATCGTAATCCAAGGGGATCCAGAAACAATGGCAGCTTTCTGGCTATTAGAGCTGCA 2713

Qy        774 AspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793

Db       2714 GATGGTACCTATATTCTGAATGGAAACTTCACTCTGTCCACTCTAGAGCAAGACCTCACC 2773

Qy        794 TyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSer 813

Db       2774 TACAAAGGTACTGTCTTAAGATACAGTGGTTCCTCAGCAGCATTGGAAAGAATCCGCAGC 2833

Qy        814 PheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArg 833

Db       2834 TTTAGTCCACTCAAAGAACCCCTGACCATCCAGGTTCTTATGGTGGGCCATGCTCTCCGA 2893

Qy        834 ProLysIleLysTyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIlePro 853

Db       2894 CCCAAAATCAAGTACACCTATTTTATGAAGAAGAAGACGGAGCCCTTCAACGCTATTCCC 2953

Qy        854 ThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGly 873

Db       2954 ACATTTTCGGAGTGGGTGATTGAAGAGTGGGGGGAGTGCTCCAAGACATGTGGTTCCGGT 3013

Qy        874 TrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893

Db       3014 TGGCAGAGGAGAGTGGTAGAGTGCAGAGACATTAATGGACACCCTGCTTCTGAATGTGCC 3073

Qy        894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGln 913

Db       3074 AAAGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGACCTTCCTTGCCCACGTTGGCAG 3133

Qy        914 LeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeu 933

Db       3134 GTGGGGGATTGGTCACCATGTTCTAAAACTTGTGGGAAGGGTTATAAGAAGACAACCTTG 3193

Qy        934 LysCysLeuSerHisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLys 953

Db       3194 AAATGTCTGTCCCATGATGGCGGTGTGTTATCAAATGAGAGCTGTGATCCTTTGAAGAAA 3253

Qy        954 ProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967

Db       3254 CCAAAGCATTACATTGACTTTTGCATACTGACACAGTGCAGT 3295
```

RESULT 12
US-10-191-803-170
; Sequence 170, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 170
; LENGTH: 4878
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_024400
US-10-191-803-170

Alignment Scores:

Pred. No.:	0	Length:	4878
Score:	4287.00	Matches:	790

Percent Similarity: 87.17% Conservative: 59
Best Local Similarity: 81.11% Mismatches: 111
Query Match: 81.09% Indels: 14
DB: 16 Gaps: 5

US-09-373-658C-126 (1-967) x US-10-191-803-170 (1-4878)

```
Qy          1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db        395 ATGCAGCCAGAAGTCCCTTTGGGGTCAGGCAAGCTGAAGCCCTGCTCAGACATGGGGGAC 454

Qy         21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db        455 ATCCAGCGGGCAGCGAAGTTTCGGAGCTCTCAGTCTGCACACATGCTGTTGCTACTCCTC 514

Qy         41 AlaAla---------LeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57
Db        515 GCTTCCATAACAATGCTGCTGTGTGTGCGGGGCGCACACGGGCGCCCCACGGAGGAAGAC 574

Qy         58 GluGluLeuValValProGluLeuGluArgValProGlyHis---GlyThrThrArgLeu 76
Db        575 GAGGAGCTGGTGCTGCCCTCGCTGGAGCGCGCCCGGGGCCACGATTCCACCACACTCCTC 634

Qy         77 ArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeu 96
Db        635 CGTCTGGACGCCTTTGGTCAGCAGCTGCATCTGAAGTTGCAGCCAGACAGCGGTTTCTTA 694

Qy         97 AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu--- 115
Db        695 GCGCCTGGCTTCACCCTCCAGACGGTGGGGCGCAGTCCTGGGTCCGAGGCACAGCATCTG 754

Qy        116 ---ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSer 134
Db        755 GACCCCACTGGGGACCTGGCCCACTGCTTCTACTCTGGCACGGTGAACGGTGACCCCAGC 814

Qy        135 SerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGlu 154
Db        815 TCCGCCGCCGCCCTCAGCCTCTGTGAAGGTGTGCGCGGTGCCTTCTACCTACAAGGCGAG 874

Qy        155 AlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThrAlaAlaPro 173
Db        875 GAGTTCTTCATTCAGCCAGCGCCTGCGGTGGCCACCGAGCGCCTGGTCCCCGCCGAACCG 934

Qy        174 GlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAsp 193
Db        935 AAGGAGGAGTCAATCGCACCTCCGCGGTTCCACATCCTGAGGCGAAGGCGGCGGGGCAGC 994

Qy        194 ValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThr 213
Db        995 GGCGGCGCAAAGTGCGGTGTCATGGACGAAGAGACCCTGCCAACC---------------- 1039

Qy        214 GluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAsp 233
Db       1040 ------AGCAACTCGGGTCGCGAAAGCCAGAACACCCCGGACCAGTGGCCTCTGCGGAAC 1093

Qy        234 ProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPhe 253
Db       1094 CCCACTCCTCAGGGCGCGGGAAAGCCAACAGGACCAGGAAGCATAAGGAAGAAGCGATTT 1153

Qy        254 ValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPhe 273
Db       1154 GTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTGGCTGACCAGTCCATGGCTGACTTC 1213

Qy        274 HisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyr 293
Db       1214 CACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTCTCGGTGGCAGCCAGATTTTAC 1273

Qy        294 LysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHis 313
Db       1274 AAGCACCCCAGCATTAGGAATTCAATTAGTCTGGTGGTGGTGAAGATCTTGGTCATATAT 1333

Qy        314 AspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCys 333
```

```
Db       1334 GAGGAGCAGAAGGGACCGGAAGTTACTTCCAATGCCGCTCTCACCCTTAGGAATTTCTGT 1393

Qy        334 AsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAla 353
Db       1394 AGCTGGCAGAAACAGCACAACAGCCCCAGTGACCGGGATCCAGAGCACTATGACACAGCG 1453

Qy        354 IleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAla 373
Db       1454 ATTCTGTTCACCAGACAGGATTTATGTGGCTCCCACACCTGTGACACTCTCGGGATGGCT 1513

Qy        374 AspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeu 393
Db       1514 GATGTTGGAACTGTATGTGACCCCAGCAGGAGCTGTTCGGTCATCGAAGATGATGGTTTA 1573

Qy        394 GlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAsp 413
Db       1574 CAGGCTGCCTTCACCACAGCCCATGAATTGGGCCATGTGTTTAACATGCCACACGATGAC 1633

Qy        414 AlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMet 433
Db       1634 GCCAAGCACTGCGCCAGCTTTAATGGCGTGAGTGGGGATTCCCATCTGATGGCCTCGATG 1693

Qy        434 LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSer 453
Db       1694 CTCTCCAGCTTGGACCACAGCCAGCCCTGGTCTCCTTGCAGTGCCTACATGGTCACATCA 1753

Qy        454 PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeu 473
Db       1754 TTCCTGGACAACGGCCATGGGGAATGTTTGATGGACAAGCCGCAGAACCCAATCAAGCTC 1813

Qy        474 ProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGly 493
Db       1814 CCATCTGATCTTCCCGGTACCTTGTACGATGCCAACCGCCAGTGTCAGTTTACCTTCGGG 1873

Qy        494 GluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGly 513
Db       1874 GAGGAATCCACGCACTGCCCTGATGCAGCCAGCACATGCAGTACCCTGTGGTGCACTGGC 1933

Qy        514 ThrSerGlyGlyValLeuValCysGlnThrLysHisProProTrpAlaAspGlyThrSer 533
Db       1934 ACCTCCGGTGGCTTACTGGTGTGCCAAACAAAACACTTCCCTTGGGCAGATGGCACCAGC 1993

Qy        534 CysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHis 553
Db       1994 TGCGGAGAAGGGAAATGGTGTGTCAGCGGCAAGTGTGTGAACAAGACCGACATGAAGCAC 2053

Qy        554 PheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArg 573
Db       2054 TTTGCTACTCCTGTTCATGGGAGCTGGGGACCGTGGGGACCATGGGGAGACTGCTCAAGA 2113

Qy        574 ThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsn 593
Db       2114 ACCTGTGGTGGAGGAGTTCAATATACAATGAGAGAATGTGACAACCCGGTCCCAAAGAAC 2173

Qy        594 GlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCys 613
Db       2174 GGGGGGAAGTACTGCGAAGGCAAACGAGTCCGCTACAGGTCCTGTAACATTGAGGACTGT 2233

Qy        614 ProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSer 633
Db       2234 CCAGACAATAACGGAAAAACATTCAGAGAGGAGCAATGCGAGGCGCACAATGAGTTTTCC 2293

Qy        634 LysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSer 653
Db       2294 AAAGCTTCCTTTGGGAATGAACCCACGGTGGAATGGACACCCAAGTATGCTGGCGTCTCG 2353

Qy        654 ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeu 673
Db       2354 CCAAAGGACAGGTGCAAGCTTACCTGCGAAGCCAAAGGCATTGGCTACTTCTTTGTTTTA 2413

Qy        674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693
Db       2414 CAGCCCAAGGTGGTAGATGGCACTCCCTGTAGTCCAGACTCTACTTCTGTCTGTGTGCAA 2473
```

```
Qy        694 GlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLys 713
Db       2474 GGACAGTGTGTGAAAGCTGGCTGTGATCGCATCATAGACTCCAAAAAGAAGTTCGATAAG 2533

Qy        714 CysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSer 733
Db       2534 TGTGGCGTTTGTGGAGGAAATGGCTCCACGTGCAAGAAAATATCAGGAACGGTCACTAGT 2593

Qy        734 AlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluVal 753
Db       2594 ACAAGACCTGGGTATCATGACATTGTCACAATTCCTGCTGGAGCCACCAACATTGAAGTG 2653

Qy        754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAla 773
Db       2654 AAACATCGTAATCCAAGGGGATCCAGAAACAATGGCAGCTTTCTGGCTATTAGAGCTGCA 2713

Qy        774 AspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793
Db       2714 GATGGTACCTATATTCTGAATGGAAACTTCACTCTGTCCACTCTAGAGCAAGACCTCACC 2773

Qy        794 TyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSer 813
Db       2774 TACAAAGGTACTGTCTTAAGATACAGTGGTTCCTCAGCAGCATTGGAAAGAATCCGCAGC 2833

Qy        814 PheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArg 833
Db       2834 TTTAGTCCACTCAAAGAACCCCTGACCATCCAGGTTCTTATGGTGGGCCATGCTCTCCGA 2893

Qy        834 ProLysIleLysTyrThrTyrPheValLysLysLysGluSerPheAsnAlaIlePro 853
Db       2894 CCCAAAATCAAGTACACCTATTTTATGAAGAAGAAGACGGAGCCCTTCAACGCTATTCCC 2953

Qy        854 ThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGly 873
Db       2954 ACATTTTCGGAGTGGGTGATTGAAGAGTGGGGGGAGTGCTCCAAGACATGTGGTTCCGGT 3013

Qy        874 TrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893
Db       3014 TGGCAGAGGAGAGTGGTAGAGTGCAGAGACATTAATGGACACCCTGCTTCTGAATGTGCC 3073

Qy        894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGln 913
Db       3074 AAAGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGACCTTCCTTGCCCACGTTGGCAG 3133

Qy        914 LeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeu 933
Db       3134 GTGGGGGATTGGTCACCATGTTCTAAAACTTGTGGGAAGGGTTATAAGAAGAGAACCTTG 3193

Qy        934 LysCysLeuSerHisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLys 953
Db       3194 AAATGTCTGTCCCATGATGGCGGTGTGTTATCAAATGAGAGCTGTGATCCTTTGAAGAAA 3253

Qy        954 ProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
Db       3254 CCAAAGCATTACATTGACTTTTGCATACTGACACAGTGCAGT 3295

RESULT 13
US-09-373-658-20
; Sequence 20, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
;  APPLICANT: Iruela-Arispe, Luisa
;  APPLICANT:  Hastings, Gregg A.
;  APPLICANT:  Ruben, Steven M.
;  APPLICANT:  Jonak, Zdenka L.
;  APPLICANT:  Trulli, Stephen H.
;  APPLICANT:  Fronwald, James A.
;  APPLICANT:  Terrett, Jonathan A.
;  TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
;  FILE REFERENCE: 1488.1070006
;  CURRENT APPLICATION NUMBER: US/09/373,658
;  CURRENT FILING DATE:  1999-08-13
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 4180
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:Unknown
US-09-373-658-20

Alignment Scores:
Pred. No.:                0                 Length:              4180
Score:                    4277.50           Matches:             789
Percent Similarity:       86.65%            Conservative:        61
Best Local Similarity:    80.43%            Mismatches:          110
Query Match:              80.91%            Indels:              21
DB:                       10                Gaps:                6

US-09-373-658C-126 (1-967) x US-09-373-658-20 (1-4180)

Qy          1 MetGlnArgAlaValPro----------------GluGlyPheGlyArgArgLysLeu 14
Db        372 GTGCAGGGTGCGGTGCCATGCAGCCAAAAGTCCCTTTTGGGGTCACGCAAGCAGAAGCCC 431

Qy         15 GlySerAspMetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValPro 34
Db        432 TGCTCCGACATGGGGGACGTCCAGCGGGCAGCGAGATCTCGGGGCTCTCTGTCCGCACAC 491

Qy         35 ThrLeuLeuLeuLeuAlaAlaAla---------LeuLeuAlaValSerAspAlaLeuGly 51
Db        492 ATGCTGTTGCTGCTCCTCGCTTCCATAACAATGCTGCTATGTGCGCGGGGCGCACACGGG 551

Qy         52 ArgProSerGluGluAspGluGluLeuValValProGluLeuGluArgValProGlyHis 71
Db        552 CGCCCCACGGAGGAAGATGAGGAGCTGGTCCTGCCCTCGCTGGAGCGCGCCCCGGGCCAC 611

Qy         72 Gly------ThrThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspVal 89
Db        612 GATTCCACCACCACACGCCTTCGTCTGGACGCCTTTGGCCAGCAGCTACATCTGAAGTTG 671

Qy         90 ProProAspSerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSer 109
Db        672 CAGCCGGACAGCGGTTTCTTGGCGCCTGGCTTCACCCTGCAGACTGTGGGGCGCAGTCCC 731

Qy        110 GlySerAspThrProLeu------ProGluThrAspLeuAlaHisCysPheTyrSerGly 127
Db        732 GGGTCCGAGGCACAACATCTGGACCCCACCGGGGACCTGGCTCACTGCTTCTACTCTGGC 791

Qy        128 ThrValAsnGlyAspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGly 147
Db        792 ACGGTGAACGGTGATCCCGGCTCTGCCGCAGCCCTCAGCCTCTGTGAAGGTGTGCGTGGT 851

Qy        148 AlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnProLeuPro---AlaAlaSerGlu 166
Db        852 GCCTTCTACCTACAAGGAGAGGAGTTCTTCATTCAGCCAGCGCCTGGAGTGGCCACCGAG 911

Qy        167 ArgLeuAlaThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeu 186
Db        912 CGCCTGGCCCCTGCCGTGCCCGAGGAGGAGTCATCCGCACGGCCGCAGTTCCACATCCTG 971

Qy        187 ArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArg 206
Db        972 AGGCGAAGGCGGCGGGGCAGTGGCGGCGCCAAGTGCGGCGTCATGGACGACGAGACCCTG 1031

Qy        207 ProThrGlyLysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGly 226
Db       1032 CCAACC--------------------AGCGACTCGCGACCCGAGAGCCAGAACACCCGG 1070

Qy        227 ProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGly 246
Db       1071 AACCAGTGGCCTGTGCGGGACCCCACGCCTCAGGACGCGGGAAAGCCATCAGGACCAGGA 1130

Qy        247 SerIleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAla 266
```


Db 1131 AGCATAAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTAGCT 1190
Qy 267 AspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPhe 286
Db 1191 GACCAGTCCATGGCCGACTTCCACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTC 1250
Qy 287 SerValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValVal 306
Db 1251 TCGGTGGCAGCCAGGTTTTACAAGCATCCCAGCATTAGGAATTCAATTAGCCTGGTGGTG 1310
Qy 307 ValLysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAla 326
Db 1311 GTGAAGATCTTGGTCATATACGAGGAGCAGAAGGGACCAGAAGTTACCTCCAATGCAGCT 1370
Qy 327 LeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAsp 346
Db 1371 CTCACCCTTCGGAATTTCTGCAGCTGGCAGAAACAACACAACAGCCCCAGTGACCGGGAT 1430
Qy 347 AlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThr 366
Db 1431 CCAGAGCACTATGACACTGCAATTCTGTTCACCAGACAGGATTTATGTGGCTCCCACACG 1490
Qy 367 CysAspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSer 386
Db 1491 TGTGACACTCTCGGAATGGCAGATGTTGGAACCGTATGTGACCCCAGCAGGAGCTGCTCA 1550
Qy 387 ValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisVal 406
Db 1551 GTCATAGAAGATGATGGTTTGCAAGCCGCCTTCACCACAGCCCATGAATTGGGCCATGTG 1610
Qy 407 PheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAsp 426
Db 1611 TTTAACATGCCGCACGATGATGCTAAGCACTGTGCCAGCTTGAATGGTGTGAGTGGCGAT 1670
Qy 427 SerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCys 446
Db 1671 TCTCATCTGATGGCCTCGATGCTCTCCAGCTTAGACCATAGCCAGCCCTGGTCACCTTGC 1730
Qy 447 SerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLys 466
Db 1731 AGTGCCTACATGGTCACGTCCTTCCTAGATAATGGACACGGGGAATGTTTGATGGACAAG 1790
Qy 467 ProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArg 486
Db 1791 CCCCAGAATCCAATCAAGCTCCCTTCTGATCTTCCCGGTACCTTGTACGATGCCAACCGC 1850
Qy 487 GlnCysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCys 506
Db 1851 CAGTGTCAGTTTACATTCGGAGAGGAATCCAAGCACTGCCCTGATGCAGCCAGCACATGT 1910
Qy 507 SerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPhe 526
Db 1911 ACTACCCTGTGGTGCACTGGCACCTCCGGTGGCTTACTGGTGTGCCAAACAAAACACTTC 1970
Qy 527 ProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysVal 546
Db 1971 CCTTGGGCAGATGGCACCAGCTGTGGAGAAGGGAAGTGGTGTGTCAGTGGCAAGTGCGTG 2030
Qy 547 AsnLysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGly 566
Db 2031 AACAAGACAGACATGAAGCATTTTGCTACTCCTGTTCATGGAAGCTGGGGACCATGGGGA 2090
Qy 567 ProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCys 586
Db 2091 CCGTGGGGAGACTGCTCAAGAACCTGTGGTGGTGGAGTTCAATACACAATGAGAGAATGT 2150
Qy 587 AspAsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArg 606
Db 2151 GACAACCCAGTCCCAAAGAACGGAGGGAAGTACTGTGAAGGCAAACGAGTCCGCTACAGG 2210
Qy 607 SerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCys 626
Db 2211 TCCTGTAACATCGAGGACTGTCCAGACAATAACGGAAAAACGTTCAGAGAGGAGCAGTGC 2270
Qy 627 GluAlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIle 646
Db 2271 GAGGCGCACAATGAGTTTTCCAAAGCTTCCTTTGGGAATGAGCCCACTGTAGAGTGGACA 2330
Qy 647 ProLysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGly 666
Db 2331 CCCAAGTACGCCGGCGTCTCGCCAAAGGACAGGTGCAAGCTCACCTGTGAAGCCAAAGGC 2390
Qy 667 IleGlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAsp 686
Db 2391 ATTGGCTACTTTTTCGTCTTACAGCCCAAGGTTGTAGATGGCACTCCCTGTAGTCCAGAC 2450
Qy 687 SerThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAsp 706
Db 2451 TCTACCTCTGTCTGTGTGCAAGGGCAGTGTGTGAAAGCTGGCTGTGATCGCATCATAGAC 2510
Qy 707 SerLysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLys 726
Db 2511 TCCAAAAAGAAGTTTGATAAGTGTGGCGTTTGTGGAGGAAACGGTTCCACATGCAAGAAG 2570
Qy 727 IleSerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThr 746
Db 2571 ATGTCAGGAATAGTCACTAGTACAAGACCTGGGTATCATGACATTGTCACAATTCCTGCT 2630
Qy 747 GlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySer 766
Db 2631 GGAGCCACCAACATTGAAGTGAAACATCGGAATCAAAGGGGGTCCAGAAACAATGGCAGC 2690
Qy 767 PheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSer 786
Db 2691 TTTCTGGCTATTAGAGCCGCTGATGGTACCTATATTCTGAATGGAAACTTCACTCTGTCC 2750
Qy 787 ThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAla 806
Db 2751 ACACTAGAGCAAGACCTCACCTACAAAGGTACTGTCTTAAGGTACAGTGGTTCCTCGGCT 2810
Qy 807 AlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeu 826
Db 2811 GCGCTGGAAAGAATCCGCAGCTTTAGTCCACTCAAAGAACCCTTAACCATCCAGGTTCTT 2870
Qy 827 ThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLys 846
Db 2871 ATGGTAGGCCATGCTCTCCGACCCAAAATTAAATTCACCTACTTTATGAAGAAGAAGACA 2930
Qy 847 GluSerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCys 866
Db 2931 GAGTCATTCAACGCCATTCCCACATTTTCTGAGTGGGTGATTGAAGAGTGGGGGGAGTGC 2990
Qy 867 SerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGly 886
Db 2991 TCCAAGACATGCGGCTCAGGTTGGCAGAGAAGAGTAGTGCAGTGCAGAGACATTAACGGA 3050
Qy 887 GlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAsp 906
Db 3051 CACCCTGCTTCCGAATGTGCAAAGGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGAC 3110
Qy 907 HisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLys 926
Db 3111 CTTCCTTGCCCACACTGGCAGGTGGGGGATTGGTCACCATGTTCCAAAACTTGCGGGAAG 3170
Qy 927 GlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAsp 946
Db 3171 GGTTACAAGAAGAGAACCTTGAAATGTGTGTCCCACGATGGGGGCGTGTTATCAAATGAG 3230
Qy 947 SerCysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCys 966
Db 3231 AGCTGTGATCCTTTGAAGAAGCCAAAGCATTACATTGACTTTTGCACACTGACACAGTGC 3290
Qy 967 Ser 967
Db 3291 AGT 3293

```
Db        862 TGGGCGGATGGCACCAGCTGTGGAGAAGGGAAATGGTGTATCAACGGCAAGTGTGTGAAC 921

Qy        548 LysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro 567

Db        922 AAAACCGACAGGAAGCATTTTGATACGCCTTTTCATGGAAGCTGGGGACCATGGGGACCG 981

Qy        568 TrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAsp 587

Db        982 TGGGGAGACTGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGAC 1041

Qy        588 AsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSer 607

Db       1042 AACCCAGTCCCAAAGAATGGAGGGAAGTACTGTGAAGGCAAACGAGTGCGCTACAGATCC 1101

Qy        608 CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGlu 627

Db       1102 TGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAACAATGTGAA 1161

Qy        628 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIlePro 647

Db       1162 GCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCCTGCGGTGGAATGGATTCCC 1221

Qy        648 LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle 667

Db       1222 AAGTACGCTGGCGTCTCACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATT 1281

Qy        668 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 687

Db       1282 GGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTTGATGGTACTCCATGTAGCCCAGATTCC 1341

Qy        688 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSer 707

Db       1342 ACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGTTGTGATCGCATCATAGACTCC 1401

Qy        708 LysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIle 727
```

```
Db       1942 CCTGCTTCCGAGTGTGCAAAGGAAGTGAAGCCAGCCAGCACCAGACCTTGTGCAGACCAT 2001

Qy        908 ProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGly 927

Db       2002 CCCTGCCCCCAGTGGCAGCTGGGGGAGTGGTCATCATGTTCTAAGACCTGTGGGAAGGGT 2061

Qy        928 TyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSer 947

Db       2062 TACAAAAAAAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGC 2121

Qy        948 CysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967

Db       2122 TGTGATCCTTTAAAGAAACCTAAACATTTCATAGACTTTTGCACACTGACACAGTGCAGT 2181
```

```
Search completed: June 18, 2004, 23:46:31
Job time : 1081.83 secs
```



```
RESULT 14
US-09-989-687-20
; Sequence 20, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
;  APPLICANT: Hastings, Gregg A.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
;  FILE REFERENCE: 1488.107000D
;  CURRENT APPLICATION NUMBER: US/09/989,687
;  CURRENT FILING DATE:  2001-11-21
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 4180
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:Unknown
US-09-989-687-20

Alignment Scores:
Pred. No.:              0               Length:         4180
Score:                  4277.50         Matches:        789
Percent Similarity:     86.65%          Conservative:   61
Best Local Similarity:  80.43%          Mismatches:     110
Query Match:            80.91%          Indels:         21
DB:                     11              Gaps:           6

US-09-373-658C-126 (1-967) x US-09-989-687-20 (1-4180)
```

```
Db        972 AGGCGAAGGCGGCGGGGCAGTGGCGGCGCCAAGTGCGGCGTCATGGACGACGAGACCCTG 1031

Qy        207 ProThrGlyLysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGly 226

Db       1032 CCAACC--------------------AGCGACTCGCGACCCGAGAGCCAGAACACCCGG 1070

Qy        227 ProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGly 246

Db       1071 AACCAGTGGCCTGTGCGGGACCCCACGCCTCAGGACGCGGGAAAGCCATCAGGACCAGGA 1130

Qy        247 SerIleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAla 266

Db       1131 AGCATAAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTCGTAGCT 1190

Qy        267 AspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPhe 286

Db       1191 GACCAGTCCATGGCCGACTTCCACGGCAGCGGTCTAAAGCATTACCTTCTAACCCTGTTC 1250

Qy        287 SerValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValVal 306

Db       1251 TCGGTGGCAGCCAGGTTTTACAAGCATCCCAGCATTAGGAATTCAATTAGCCTGGTGGTG 1310

Qy        307 ValLysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAla 326

Db       1311 GTGAAGATCTTGGTCATATACGAGGAGCAGAAGGGACCAGAAGTTACCTCCAATGCAGCT 1370

Qy        327 LeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAsp 346

Db       1371 CTCACCCTTCGGAATTTCTGCAGCTGGCAGAAACAACACAACAGCCCCAGTGACCGGGAT 1430

Qy        347 AlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThr 366
```

```
Qy        747 GlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySer 766
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db       2631 GGAGCCACCAACATTGAAGTGAAACATCGGAATCAAAGGGGGTCCAGAAACAATGGCAGC 2690

Qy        767 PheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSer 786
              ||||||||||:::|||||||||||||||||||||||||||||||:::::|||||||||
Db       2691 TTTCTGGCTATTAGAGCCGCTGATGGTACCTATATTCTGAATGGAAACTTCACTCTGTCC 2750

Qy        787 ThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAla 806
              ||||||||||||||:::   |||||||||  ||||||||||||||||||||||||||||
Db       2751 ACACTAGAGCAAGACCTCACCTACAAAGGTACTGTCTTAAGGTACAGTGGTTCCTCGGCT 2810

Qy        807 AlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeu 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2811 GCGCTGGAAAGAATCCGCAGCTTTAGTCCACTCAAAGAACCCTTAACCATCCAGGTTCTT 2870

Qy        827 ThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLys 846
              |||||||:::|||||||||||||||||||:::|||||||||:::|||||||||
Db       2871 ATGGTAGGCCATGCTCTCCGACCCAAAATTAAATTCACCTACTTTATGAAGAAGAAGACA 2930

Qy        847 GluSerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCys 866
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db       2931 GAGTCATTCAACGCCATTCCCACATTTTCTGAGTGGGTGATTGAAGAGTGGGGGGAGTGC 2990

Qy        867 SerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGly 886
              ||||||:::|||       ||||||||||||||:::|||:::|||||||||||||||||
Db       2991 TCCAAGACATGCGGCTCAGGTTGGCAGAGAAGAGTAGTGCAGTGCAGAGACATTAACGGA 3050

Qy        887 GlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAsp 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3051 CACCCTGCTTCCGAATGTGCAAAGGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGAC 3110

Qy        907 HisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLys 926
              |||||||||   ||||||:::|||:::|||||   ||||||||||||||||||||||||
Db       3111 CTTCCTTGCCCACACTGGCAGGTGGGGGATTGGTCACCATGTTCCAAAACTTGCGGGAAG 3170
```

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(2184)
US-09-445-023A-2

Alignment Scores:
Pred. No.:                0                Length:          2184
Score:                    3922.00          Matches:         707
Percent Similarity:       98.89%           Conservative:    5
Best Local Similarity:    98.19%           Mismatches:      8
Query Match:              74.18%           Indels:          0
DB:                       9                Gaps:            0

US-09-373-658C-126 (1-967) x US-09-445-023A-2 (1-2184)

Qy        248 IleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAsp 267
              :::|||||||||||||||||||||||||    |||||||||||||||||||||||||||||
Db         22 CTTAGGAAGAAGCGATTTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTTGTGGCAGAC 81

Qy        268 GlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSer 287
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAGTCGATGGCAGAATTCCACGGCAGTGGTCTAAAGCATTACCTTCTCACGTTGTTTTCG 141

Qy        288 ValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVal 307
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 GTGGCAGCCAGATTGTACAAACACCCCAGCATTCGTAATTCAGTTAGCCTGGTGGTGGTG 201

Qy        308 LysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeu 327
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAGATCTTGGTCATCCACGATGAACAGAAGGGGCCGGAAGTGACCTCCAATGCTGCCCTC 261

Qy        328 ThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAla 347
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 ACTCTGCGGAACTTTTGCAACTGGCAGAAGCAGCACAACCCACCCAGTGACCGGGATGCA 321
```